```
=> fil reg; d que l5
FILE 'REGISTRY' ENTERED AT 11:04:52 ON 26 JAN 2006
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STRUCTURE FILE UPDATES:   25 JAN 2006  HIGHEST RN 872674-04-9
DICTIONARY FILE UPDATES:  25 JAN 2006  HIGHEST RN 872674-04-9

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*************************************************************************
*                                                                       *
* The CA roles and document type information have been removed from     *
* the IDE default display format and the ED field has been added,       *
* effective March 20, 2005.  A new display format, IDERL, is now        *
* available and contains the CA role and document type information.     *
*                                                                       *
*************************************************************************

Structure search iteration limits have been increased.  See HELP SLIMITS
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REGISTRY includes numerically searchable data for experimental and
predicted properties as well as tags indicating availability of
experimental property data in the original document.  For information
on property searching in REGISTRY, refer to:

http://www.cas.org/ONLINE/UG/regprops.html


L2            1041 SEA FILE=REGISTRY ABB=ON  CCCUGUGAGGAACUWCUGUCU|AGACAGSAGUUCCUC
                   ACAGGG|GCAAGUGCUGUAGGUGCGGGG|CCCCGCACCUACAGCACUUGC/SQSN
L3              46 SEA FILE=REGISTRY ABB=ON  L2 AND SQL<101
L5              26 SEA FILE=REGISTRY ABB=ON  L3 NOT GENBANK/LC


=> d rn cn kwic nte lc l5 1-26; fil capl uspatf toxcenter; s l5

L5   ANSWER 1 OF 26  REGISTRY  COPYRIGHT 2006 ACS on STN
RN   851551-44-5  REGISTRY
CN   2: PN: CN1460722 SEQID: 2 claimed DNA (9CI)  (CA INDEX NAME)
SQL  95

SEQ      1 cgaaattaat acgactcact atagggccac catagatcac tcccctgtga
                                                    ========
        51 ggaactactg tcttcacgca gaaagcgtct agccatggcg ttagt
           ========== ===
HITS AT:   43-63
LC   STN Files:   CA, CAPLUS

L5   ANSWER 2 OF 26  REGISTRY  COPYRIGHT 2006 ACS on STN
```

RN 851551-43-4 REGISTRY
CN 1: PN: CN1460722 SEQID: 1 claimed RNA (9CI) (CA INDEX NAME)
SQL **70**

SEQ 1 gccaccauag aucacucccc ugugaggaac uacugucuuc acgcagaaag
=== ========== ========
HITS AT: 18-38
LC STN Files: CA, CAPLUS

L5 ANSWER 3 OF 26 REGISTRY COPYRIGHT 2006 ACS on STN
RN 850271-03-3 REGISTRY
CN DNA, d(C-C-C-T-G-T-G-A-G-G-A-A-C-T-W-C-T-G-T-C-T-T-C-A-C-G-C) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 4: PN: CN1477209 SEQID: 4 claimed DNA
SQL **27**

SEQ 1 ccctgtgagg aactwctgtc ttcacgc
========== ========== =
HITS AT: 1-21

RELATED SEQUENCES AVAILABLE WITH SEQLINK
LC STN Files: CA, CAPLUS

L5 ANSWER 4 OF 26 REGISTRY COPYRIGHT 2006 ACS on STN
RN 800937-98-8 REGISTRY
CN DNA, d(C-C-C-C-T-G-T-G-A-G-G-A-A-C-T-A-C-T-G-T-C-T-T-C-A-C-G-C) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 20: PN: WO2004104198 SEQID: 19 unclaimed DNA
SQL **28**

SEQ 1 cccctgtgag gaactactgt cttcacgc
========= ========== ==
HITS AT: 2-22
LC STN Files: CA, CAPLUS

L5 ANSWER 5 OF 26 REGISTRY COPYRIGHT 2006 ACS on STN
RN 760219-09-8 REGISTRY
CN DNA, d(A-C-T-C-C-C-C-T-G-T-G-A-G-G-A-A-C-T-A-C-T-G-T-C-T) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 35: PN: WO2004078974 SEQID: 35 unclaimed DNA
SQL **25**

SEQ 1 actcccctgt gaggaactac tgtct
====== ========== =====
HITS AT: 5-25
LC STN Files: CA, CAPLUS

L5 ANSWER 6 OF 26 REGISTRY COPYRIGHT 2006 ACS on STN
RN 735853-91-5 REGISTRY
CN DNA, d(C-C-C-T-G-T-G-A-G-G-A-A-C-T-A-C-T-G-T-C-T-T-T-C-A-C-G) (9CI) (CA INDEX NAME)
SQL **27**

SEQ 1 ccctgtgagg aactactgtc tttcacg
========== ========== =
HITS AT: 1-21
LC STN Files: CA, CAPLUS

L5 ANSWER 7 OF 26 REGISTRY COPYRIGHT 2006 ACS on STN
RN [redacted] REGISTRY
CN DNA (hepatitis C virus internal ribosome entry site region II) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 72: PN: FR2848572 SEQID: 2 claimed DNA
SQL 80

SEQ 1 ctcccctgtg aggaactact gtcttcacgc agaaagcgtc tagccatggc
======= ========== ====
HITS AT: 4-24

RELATED SEQUENCES AVAILABLE WITH SEQLINK
LC STN Files: CA, CAPLUS

L5 ANSWER 8 OF 26 REGISTRY COPYRIGHT 2006 ACS on STN
RN [redacted] REGISTRY
CN RNA, (C-C-C-U-G-U-G-A-G-G-A-A-C-U-A-C-U-G-U-C-U-U-C) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 20: PN: WO2004011647 FIGURE: 2 unclaimed sequence
SQL 23

SEQ 1 cccugugagg aacuacuguc uuc
========== ========== =
HITS AT: 1-21
LC STN Files: CA, CAPLUS, USPATFULL

L5 ANSWER 9 OF 26 REGISTRY COPYRIGHT 2006 ACS on STN
RN [redacted] REGISTRY
CN DNA, d(C-C-C-T-G-T-G-A-G-G-A-A-C-T-A-C-T-G-T-C-T-T-C-A-C-G) (9CI) (CA INDEX NAME)
SQL 26

SEQ 1 ccctgtgagg aactactgtc ttcacg
========== ========== =
HITS AT: 1-21
LC STN Files: CA, CAPLUS

L5 ANSWER 10 OF 26 REGISTRY COPYRIGHT 2006 ACS on STN
RN [redacted] REGISTRY
CN DNA, d(C-C-C-T-G-T-G-A-G-G-A-A-C-T-W-C-T-G-T-C-T-T-C-A-C-G-C) (9CI) (CA INDEX NAME)
SQL 27

SEQ 1 ccctgtgagg aactwctgtc ttcacgc
========== ========== =
HITS AT: 1-21

RELATED SEQUENCES AVAILABLE WITH SEQLINK
LC STN Files: CA, CAPLUS

L5 ANSWER 11 OF 26 REGISTRY COPYRIGHT 2006 ACS on STN
RN [redacted] REGISTRY
CN DNA, d(C-C-C-T-G-T-G-A-G-G-A-A-C-T-A-C-T-G-T-C-T-T-C-A-C-G-C) (9CI) (CA INDEX NAME)
SQL 27

SEQ 1 ccctgtgagg aactactgtc ttcacgc

```
          ========== ========== =
HITS AT:   1-21

**RELATED SEQUENCES AVAILABLE WITH SEQLINK**
LC   STN Files:   CA, CAPLUS

L5   ANSWER 12 OF 26  REGISTRY  COPYRIGHT 2006 ACS on STN
RN   465577-45-1  REGISTRY
CN   DNA, d(C-C-C-T-G-T-G-A-G-G-A-A-C-T-W-C-T-G-T-C-T) (9CI)  (CA INDEX NAME)
OTHER NAMES:
CN   1: PN: WO02077281 SEQID: 1 claimed DNA
SQL  21

SEQ      1 ccctgtgagg aactwctgtc t
           ========== ========== =
HITS AT:   1-21

**RELATED SEQUENCES AVAILABLE WITH SEQLINK**
LC   STN Files:   CA, CAPLUS, USPATFULL

L5   ANSWER 13 OF 26  REGISTRY  COPYRIGHT 2006 ACS on STN
RN   459459-16-6  REGISTRY
CN   DNA, d(C-A-C-T-C-C-C-C-T-G-T-G-A-G-G-A-A-C-T-A-C-T-G-T-C-T) (9CI)  (CA
     INDEX NAME)
SQL  26

SEQ      1 cactcccctg tgaggaacta ctgtct
               ===== ========== ======
HITS AT:   6-26

**RELATED SEQUENCES AVAILABLE WITH SEQLINK**
LC   STN Files:   CA, CAPLUS

L5   ANSWER 14 OF 26  REGISTRY  COPYRIGHT 2006 ACS on STN
RN   440077-63-4  REGISTRY
CN   41: PN: WO02052043 SEQID: 41 unclaimed DNA (9CI)  (CA INDEX NAME)
SQL  73

SEQ      1 cactccacca tgaatcactc ccctgtgagg aactactgtc ttcacgcaga
                                 ========== ========== =
HITS AT:   21-41

**RELATED SEQUENCES AVAILABLE WITH SEQLINK**
LC   STN Files:   CA, CAPLUS, USPATFULL

L5   ANSWER 15 OF 26  REGISTRY  COPYRIGHT 2006 ACS on STN
RN   439889-66-4  REGISTRY
CN   DNA, d(C-C-C-T-G-T-G-A-G-G-A-A-C-T-A-C-T-G-T-C-T-T-C-A) (9CI)  (CA INDEX
     NAME)
OTHER NAMES:
CN   1: PN: WO02052041 SEQID: 1 unclaimed DNA
SQL  24

SEQ      1 ccctgtgagg aactactgtc ttca
           ========== ========== =
HITS AT:   1-21

**RELATED SEQUENCES AVAILABLE WITH SEQLINK**
LC   STN Files:   CA, CAPLUS, USPATFULL
```

L5 ANSWER 16 OF 26 REGISTRY COPYRIGHT 2006 ACS on STN
RN 404885-02-5 REGISTRY
CN DNA, d(C-C-C-T-G-T-G-A-G-G-A-A-C-T-A-C-T-G-T-C-T-T-C-A-C-G-C) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 5: PN: RU2163638 SEQID: 5 claimed DNA
SQL **27**

SEQ 1 ccctgtgagg aactactgtc ttcacgc SID 1
========== ========== =
HITS AT: 1-21

RELATED SEQUENCES AVAILABLE WITH SEQLINK
LC STN Files: CA, CAPLUS, TOXCENTER

L5 ANSWER 17 OF 26 REGISTRY COPYRIGHT 2006 ACS on STN
RN 404321-95-5 REGISTRY
CN DNA, d(C-C-C-T-G-T-G-A-G-G-A-A-C-T-W-C-T-G-T-C-T-T-C-A-C-G-C) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 1: PN: WO0220837 PAGE: 43 unclaimed DNA
SQL **27**

SEQ 1 ccctgtgagg aactwctgtc ttcacgc
========== ========== =
HITS AT: 1-21

RELATED SEQUENCES AVAILABLE WITH SEQLINK
LC STN Files: CA, CAPLUS, USPATFULL

L5 ANSWER 18 OF 26 REGISTRY COPYRIGHT 2006 ACS on STN
RN 393599-90-1 REGISTRY
CN 28: PN: WO0208447 SEQID: 28 unclaimed DNA (9CI) (CA INDEX NAME)
SQL **85**

SEQ 1 gccagccccc gattgggggc gacactccac catagatcac tcccctgtga
========
51 ggaactactg tcttcacgca gaaagcgtct agcca
========== ===
HITS AT: 43-63
LC STN Files: CA, CAPLUS, USPATFULL

L5 ANSWER 19 OF 26 REGISTRY COPYRIGHT 2006 ACS on STN
RN 259204-93-8 REGISTRY
CN DNA, d(C-T-C-C-C-C-T-G-T-G-A-G-G-A-A-C-T-A-C-T-G-T-C-T-T) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 1: PN: WO0009745 SEQID: 1 claimed DNA
SQL **25**

SEQ 1 ctcccctgtg aggaactact gtctt
======= ========== ====
HITS AT: 4-24

RELATED SEQUENCES AVAILABLE WITH SEQLINK
LC STN Files: CA, CAPLUS, USPAT2, USPATFULL

L5 ANSWER 20 OF 26 REGISTRY COPYRIGHT 2006 ACS on STN
RN 253656-91-6 REGISTRY
CN 13: PN: EP969101 PAGE: 23/24 unclaimed DNA (9CI) (CA INDEX NAME)

SQL **71**

```
SEQ      1 uuggggcga cacuccacca uagaucacuc cccugugagg aacuacuguc
                                          ========== ==========
        51 uucacgcaga aagcgucuag c
           =
HITS AT:   31-51
LC   STN Files:   CA, CAPLUS, USPATFULL
```

L5 ANSWER 21 OF 26 REGISTRY COPYRIGHT 2006 ACS on STN
RN 252853-10-4 REGISTRY
CN DNA, d(C-A-C-T-C-C-C-C-T-G-T-G-A-G-G-A-A-C-T-A-C-T-G-T-C-T-T-C) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 29: PN: US6001990 SEQID: 29 claimed DNA
SQL **28**

```
SEQ      1 cactcccctg tgaggaacta ctgtcttc
               ===== ========== ======
HITS AT:   6-26
```

RELATED SEQUENCES AVAILABLE WITH SEQLINK
LC STN Files: CA, CAPLUS, USPATFULL

L5 ANSWER 22 OF 26 REGISTRY COPYRIGHT 2006 ACS on STN
RN 227013-13-0 REGISTRY
CN DNA, d(C-C-C-C-T-G-T-G-A-G-G-A-A-C-T-A-C-T-G-T-C-T-T-C) (9CI) (CA INDEX NAME)
SQL **24**

```
SEQ      1 cccctgtgag gaactactgt cttc
            ========= ========== ==
HITS AT:   2-22
```

RELATED SEQUENCES AVAILABLE WITH SEQLINK
LC STN Files: CA, CAPLUS

L5 ANSWER 23 OF 26 REGISTRY COPYRIGHT 2006 ACS on STN
RN 182895-29-0 REGISTRY
CN DNA, d(C-A-C-T-C-C-C-C-T-G-T-G-A-G-G-A-A-C-T-A-C-T-G-T-C-T) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Deoxyribonucleic acid, d(C-A-C-T-C-C-C-C-T-G-T-G-A-G-G-A-A-C-T-A-C-T-G-T-C-T)
SQL **26**

```
SEQ      1 cactcccctg tgaggaacta ctgtct
               ===== ========== ======
HITS AT:   6-26
```

RELATED SEQUENCES AVAILABLE WITH SEQLINK
LC STN Files: CA, CAPLUS

L5 ANSWER 24 OF 26 REGISTRY COPYRIGHT 2006 ACS on STN
RN 171761-22-1 REGISTRY
CN DNA, d(B-C-C-C-T-G-T-G-A-G-G-A-A-C-T-W-C-T-G-T-C-T-T-C-A-C-G-C) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Deoxyribonucleic acid, d(B-C-C-C-T-G-T-G-A-G-G-A-A-C-T-W-C-T-G-T-C-T-T-C-A-C-G-C)

SQL **28**

SEQ 1 bccctgtgag gaactwctgt cttcacgc
========== ========== ==
HITS AT: 2-22
NTE singlestranded
LC STN Files: CA, CAPLUS

L5 ANSWER 25 OF 26 REGISTRY COPYRIGHT 2006 ACS on STN
RN 159942-56-0 REGISTRY
CN DNA, d(C-A-C-T-C-C-C-C-T-G-T-G-A-G-G-A-A-C-T-A-C-T-G-T-C-T-T-C-A-C-G-C-A-G-A-A-A-G-C-G-T-C-T-A-G-C-C-A-T-G-G-C-G-T-T-A-G-T-A-T-G-A-G-T-G-T-C-G-T) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Deoxyribonucleic acid, d(C-A-C-T-C-C-C-C-T-G-T-G-A-G-G-A-A-C-T-A-C-T-G-T-C-T-T-C-A-C-G-C-A-G-A-A-A-G-C-G-T-C-T-A-G-C-C-A-T-G-G-C-G-T-T-A-G-T-A-T-G-A-G-T-G-T-C-G-T)
SQL **69**

SEQ 1 cactcccctg tgaggaacta ctgtcttcac gcagaaagcg tctagccatg
===== ========== ======
HITS AT: 6-26
NTE singlestranded
LC STN Files: CA, CAPLUS

L5 ANSWER 26 OF 26 REGISTRY COPYRIGHT 2006 ACS on STN
RN 157607-57-3 REGISTRY
CN DNA, d(C-C-C-T-G-T-G-A-G-G-A-A-C-T-W-C-T-G-T-C-T-T-C-A-C-G-C) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Deoxyribonucleic acid, d(C-C-C-T-G-T-G-A-G-G-A-A-C-T-W-C-T-G-T-C-T-T-C-A-C-G-C)
OTHER NAMES:
CN 86: PN: WO0136442 PAGE: 16 unclaimed sequence
SQL **27**

SEQ 1 ccctgtgagg aactwctgtc ttcacgc
========== ========== =
HITS AT: 1-21

RELATED SEQUENCES AVAILABLE WITH SEQLINK
LC STN Files: CA, CAPLUS, USPAT2, USPATFULL

FILE 'CAPLUS' ENTERED AT 11:05:40 ON 26 JAN 2006
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FILE 'USPATFULL' ENTERED AT 11:05:40 ON 26 JAN 2006
CA INDEXING COPYRIGHT (C) 2006 AMERICAN CHEMICAL SOCIETY (ACS)

FILE 'TOXCENTER' ENTERED AT 11:05:40 ON 26 JAN 2006
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L6 48 L5

=> dup rem l6

PROCESSING COMPLETED FOR L6
L7 46 DUP REM L6 (2 DUPLICATES REMOVED)
ANSWERS '1-26' FROM FILE CAPLUS
ANSWERS '27-46' FROM FILE USPATFULL

=> d ibib ed abs hitrn 1-46; fil hom

L7 ANSWER 1 OF 46 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 1
ACCESSION NUMBER: 2002:259256 CAPLUS
DOCUMENT NUMBER: 136:258260
TITLE: PCR-based method and reagent kit for detection of DNA of tuberculosis mycobacteria with differential detection of Mycobacterium tuberculosis
INVENTOR(S): Beklemishev, A. B.; Khorosheva, E. M.; Nomokonova, N. Yu.
PATENT ASSIGNEE(S): Nauchno-Issledovatel'skii Institut Biokhimii So Ramn, Russia
SOURCE: Russ., No pp. given
CODEN: RUXXE7
DOCUMENT TYPE: Patent
LANGUAGE: Russian
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
RU 2163638	C1	20010227	RU 1999-125164	19991206
PRIORITY APPLN. INFO.:			RU 1999-125164	19991206

ED Entered STN: 09 Apr 2002
AB The present invention relates to mol. biol. medicines and veterinary science and designated for detection of tuberculosis mycobacterium complex where species Mycobacterium tuberculosis, M. bovis, M. microti and M. africanum belong. The invention proposes improved method of detection and provides set based on a single-round multiprimer polycyclic amplification by polymerase chain reaction (PCR) in total reaction mixture The latter has, in part, glycerol, two targets of genome DNA and nucleotide sequence as an internal standard This ensures to estimate effectiveness of PCR on DNA of the sample to be analyzed and eliminate false-neg. data of anal. One of taken target is fragment of RD1 genomes that is typical for all species of tuberculosis mycobacterium complex (with exception for M. bovis BCG) involving gene site that encodes protein ESAT-6; the second target is fragment of gene mtp-40 showing specificity for M. tuberculosis. Proposed set has: (1) concentrated reaction mixture; (2) thermostable DNA-polymerase (5 U/mcl); (3) ionized sterile water; (4) mineral oil; (5) (+)-control DNA (M. tuberculosis DNA). Invention ensures to carry out differential detection of mycobacteria of species M. tuberculosis among other species of tuberculosis mycobacterium complex and reveal the above indicated mycobacteria in biol. specimens obtained from humans, agriculture and wild animals, estimate effectiveness of therapy and disinfection measure.
IT **404885-02-5**
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(M. tuberculosis control standard, f-p60-k; PCR-based method and reagent kit for detection of DNA of tuberculosis mycobacteria with differential detection of M. tuberculosis)

L7 ANSWER 2 OF 46 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 2
ACCESSION NUMBER: 1999:794368 CAPLUS
DOCUMENT NUMBER: 132:44954

TITLE: Antisense inhibition of hepatitis C virus-specific RNA translation
INVENTOR(S): Wands, Jack R.; Wakita, Takaja; Moradpour, Darius
PATENT ASSIGNEE(S): The General Hospital Corporation, USA
SOURCE: U.S., 31 pp., Cont.-in-part of U.S. Ser. No. 240,382, abandoned.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 6001990	A	19991214	US 1995-474700	19950607
PRIORITY APPLN. INFO.:			US 1994-240382	B2 19940510

ED Entered STN: 16 Dec 1999
AB The invention features antisense oligonucleotides and methods of using these antisense oligonucleotides for inhibiting HCV RNA translation.
IT 252853-10-4
RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PROC (Process); USES (Uses)
(antisense inhibition of hepatitis C virus-specific RNA translation)
REFERENCE COUNT: 76 THERE ARE 76 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 3 OF 46 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2004:1037242 CAPLUS
DOCUMENT NUMBER: 142:18452
TITLE: Hepatitis C virus genotype 2a subgenomic replicon and uses in diagnosis, therapy, and drug screening
INVENTOR(S): Wakita, Takaji; Kato, Takanobu; Date, Tomoko
PATENT ASSIGNEE(S): Toray Industries, Inc., Japan; Tokyo Metropolitan Organization for Medical Research; Johannes Gutenberg-Universitaet Mainz
SOURCE: PCT Int. Appl., 197 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2004104198	A1	20041202	WO 2003-JP15038	20031125

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW
RW: BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.:	JP 2003-148242	A	20030526
	JP 2003-329115	A	20030919

ED Entered STN: 03 Dec 2004
AB Replicon comprising a sequence containing 5'-untranslated region (5'-UTR),

sequences encoding NS3 protein, NS4A protein, NS4B protein, NS5A protein and NS5B protein and 3'-untranslated region (3'-UTR) of the genomic RNA of hepatitis C virus of genotype 2a, is provided. HCV replicon also contains selection marker gene, a reporter gene, and IRES sequence. Use of the replicon for preparation of therapeutic or diagnostic agents for HCV virus infection, or vaccines, and screening of agents that promote or inhibit HCV virus replication, is claimed. Although the hepatitis C virus (HCV) subgenomic replicon system has been widely used in the study of HCV, this system is available only for a few related genotypes. A genotype 2a replicon was constructed by isolating the consensus sequence of JFH-1, transfecting G418-selectable subgenomic transcripts into Huh7 cells, and estimating the replication efficiency. The JFH-1 replicon RNA was transmissible to naive Huh7 cells by transfection of cellular RNA from cells containing the replicon. Sequencing of cloned replicon RNAs revealed that all but 1 had at least 1 non-synonymous mutation. One of these mutations was shown to enhance the colony formation efficiency of the JFH-1 replicon. The genotype 2a subgenomic replicon was established in Huh7 cells and replicated efficiently with or without G418 selection. Also the replication of JFH-1 replicon was tested in HepG2, a human hepatocyte-derived cell line, and in IMY-N9, a cell line developed by fusing human hepatocytes and HepG2 cells. Following transfection with in vitro transcribed replicon RNA and selection by cultivation with G418, colonies formed in both cell lines although at efficiencies substantially lower than those of Huh7. The H2476L mutation identified in the Huh7 replicon in our previous study increased the colony formation efficiencies of the JFH-1 replicon in HepG2 and IMY-N9 cells. This system with the JFH-1 replicon and three cell lines is useful not only for estimating the cellular factors affecting viral activity but also for clarifying the common gene response of the host.

IT **800937-98-8**
RL: PRP (Properties)
(unclaimed nucleotide sequence; hepatitis C virus genotype 2a subgenomic replicon and uses in diagnosis, therapy, and drug screening)

REFERENCE COUNT: 12 THERE ARE 12 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 4 OF 46 CAPLUS COPYRIGHT 2006 ACS on STN

ACCESSION NUMBER: 2004:756878 CAPLUS
DOCUMENT NUMBER: 141:272579
TITLE: Oligoribonucleotide for inhibiting HCV multiplication by RNA interference
INVENTOR(S): Kohara, Michinori; Watanabe, Tsunamasa; Taira, Kazunari; Miyagishi, Makoto; Sudo, Masayuki
PATENT ASSIGNEE(S): Tokyo Metropolitan Organization for Medical Research, Japan; Chugai Seiyaku Kabushiki Kaisha
SOURCE: PCT Int. Appl., 80 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2004078974	A1	20040916	WO 2004-JP605	20040123

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI
RW: BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE,

BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

EP 1591524 A1 20051102 EP 2004-704739 20040123
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, SK

PRIORITY APPLN. INFO.: JP 2003-16750 A 20030124
WO 2004-JP605 W 20040123

ED Entered STN: 16 Sep 2004

AB This invention provides a method of inhibiting the multiplication of Hepatitis C virus (HCV) by RNA interference. The invention also provides the sequences of siRNA targeting 5'-UTR of HCV-RNA. The method provided in this invention can be used for treatment of hepatitis C.

IT 760219-09-8
RL: PRP (Properties)
(unclaimed nucleotide sequence; oligoribonucleotide for inhibiting HCV multiplication by RNA interference)

REFERENCE COUNT: 12 THERE ARE 12 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 5 OF 46 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2004:101300 CAPLUS
DOCUMENT NUMBER: 140:157419
TITLE: Small interfering RNAs with backbone or base modifications directed against hepatitis C virus and their use in treatment of infection
INVENTOR(S): Han, Jang; Seo, Mi Young; Houghton, Michael
PATENT ASSIGNEE(S): Chiron Corporation, USA
SOURCE: PCT Int. Appl., 74 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2004011647	A1	20040205	WO 2003-US23104	20030725
WO 2004011647	C1	20040610		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

CA 2493949	AA	20040205	CA 2003-2493949	20030725
US 2005058982	A1	20050317	US 2003-626879	20030725
EP 1532248	A1	20050525	EP 2003-771767	20030725

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, SK

JP 2005533517	T2	20051110	JP 2004-524748	20030725

PRIORITY APPLN. INFO.:

US 2002-398605P	P	20020726
US 2003-461838P	P	20030411
US 2003-470230P	P	20030514
WO 2003-US23104	W	20030725

ED Entered STN: 08 Feb 2004

AB Small interfering RNAs that interfere with the expression of hepatitis C virus genes in target cells, preferably hepatic cells are described. These RNAs may have modified backbones that are resistant to nuclease degradation The invention also provides a method of using these modified RNA mols. to inactivate virus in mammalian cells and method of making modified small interfering RNAs (siRNAs) using human Dicer.

IT **654887-99-7**
RL: PRP (Properties)
(unclaimed sequence; small interfering RNAs with backbone or base modifications directed against hepatitis C virus and their use in treatment of infection)

REFERENCE COUNT: 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 6 OF 46 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2004:492339 CAPLUS
DOCUMENT NUMBER: 141:47284
TITLE: Methods for the screening of modulators of hepatitis C virus (HCV) protein synthesis and therapeutic uses thereof
INVENTOR(S): Balakireva, Larissa
PATENT ASSIGNEE(S): Universite Joseph Fourier, Fr.
SOURCE: Fr. Demande, 45 pp.
CODEN: FRXXBL
DOCUMENT TYPE: Patent
LANGUAGE: French
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
FR 2848572	A1	20040618	FR 2002-15718	20021212
FR 2848572	B1	20051209		
WO 2004055210	A1	20040701	WO 2003-FR3675	20031211
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW				
RW: BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
EP 1570089	A1	20050907	EP 2003-813166	20031211
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, SK				

PRIORITY APPLN. INFO.: FR 2002-15718 A 20021212
WO 2003-FR3675 W 20031211

ED Entered STN: 18 Jun 2004
AB Method for the screening mols. according to which, in vitro: (A) one incubates together the eukaryotic translation initiation factor 3 (eIF3) subunit p110 (SEQ ID4), the nucleic sequence of hepatitis C virus internal ribosome entry site (IRES) region II (SEQ ID2) or any sequence containing at least 10 successive nucleotides of IRES region II (SEQ ID2) and the mol. to be tested, (B) one detects then the possible complex formation between p110 and IRES region II, the absence of complex signifying an inhibiting capacity of the mol. tested to inhibit the formation of the aforesaid complex, and (C) one selects the mols. inhibiting the formation of the complexes. Such selected mols. can then be used therapeutically in the

treatment of infection with virus presenting a similar IRES region II to that of HCV, such as hog cholera virus and bovine diarrhea virus.

IT 708296-81-5

RL: BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(nucleotide sequence; mols. inhibiting the protein synthesis of hepatitis C virus and method for screening of inhibiting mols.)

REFERENCE COUNT: 9 THERE ARE 9 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 7 OF 46 CAPLUS COPYRIGHT 2006 ACS on STN

ACCESSION NUMBER: 2004:1149123 CAPLUS
DOCUMENT NUMBER: 142:405493
TITLE: Immobilized probes for detection of hepatitis C virus genotype and its use for diagnosis
INVENTOR(S): Zhao, Jianlong; Mao, Hongju; Yuan, Zhenghong; Liu, Jiangxia; Zhao, Hui; Zhang, Hua; Xu, Yuansen
PATENT ASSIGNEE(S): Shanghai Institute of Microsystems and Information Technology, Chinese Academy of Sciences, Peop. Rep. China
SOURCE: Faming Zhuanli Shenqing Gongkai Shuomingshu, 16 pp. CODEN: CNXXEV
DOCUMENT TYPE: Patent
LANGUAGE: Chinese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
CN 1477209	A	20040225	CN 2003-141631	20030716

PRIORITY APPLN. INFO.: CN 2003-141631 20030716
ED Entered STN: 29 Dec 2004
AB This invention provides a method of immobilization of probes for detection of hepatitis C virus genotype. The method comprises immobilizing the oligonucleotide probes for hepatitis C virus on aldehyde-modified glass plate, hybridizing with digoxin- or biotin-labeled PCR products, and adding alkaline phosphatase-labeled anti-digoxin antibody or avidin-labeled antibody. The method provided in this invention can be used for diagnosis of hepatitis C.

IT 850271-03-3

RL: BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); BIOL (Biological study); USES (Uses)
(nucleic acid; immobilized probes for detection of hepatitis C virus genotype and its use for diagnosis)

L7 ANSWER 8 OF 46 CAPLUS COPYRIGHT 2006 ACS on STN

ACCESSION NUMBER: 2004:363056 CAPLUS
DOCUMENT NUMBER: 141:168590
TITLE: Improved detection of HCV Infection in hemodialysis patients using a new HCV RNA qualitative assay: experience of a transplant center
AUTHOR(S): Khan, Nasreen; Aswad, Sali; Shidban, Hamid; Aghajani, Mehbobeh; Mendez, Ralph; Mendez, Robert; Comanor, Lorraine
CORPORATE SOURCE: National Institute of Transplantation, Los Angeles, CA, USA
SOURCE: Journal of Clinical Virology (2004), 30(2), 175-182 CODEN: JCVIFB; ISSN: 1386-6532
PUBLISHER: Elsevier B.V.
DOCUMENT TYPE: Journal

LANGUAGE: English
ED Entered STN: 04 May 2004
AB Hepatitis C virus (HCV) is frequently a silent infection in hemodialysis (HD) patients with a prevalence of 8-10%. Improving HCV detection in this population prior to transplantation is critical both for infection control and optimal patient care. The objective of this study was to assess the current HCV testing practice of the National Institute for Transplantation, which involves PCR testing of enzyme immunoassay (EIA) pos. HD patients. Specifically, a subset of EIA pos. and EIA neg. samples were evaluated using VERSANT HCV RNA Qual. Assay based on transcription mediated amplification (HCV Qual (TMA)) (sensitivity ≤9.6 IU/mL) and inhouse PCR (HCV Qual (PCR)) (sensitivity .apprx.149 IU/mL). 2321 HD patients were screened by Abbott HCV EIA 2.0. A subset of 80/169 E IA pos. samples and 100/2152 EIA neg. samples were tested by both assays. TMA/PCR discordant samples were genotyped. The results revealed PCR and TMA gave concordant results in 67/80 (83.8%) of EIA pos. samples. 11/80 (14.7%) Were reactive by HCV Qual (TMA), but not by HCV Qual (PCR); 2/80 (2.7%) were reactive by HCV Qual (PCR), but not by HCV Qual (TMA). 2/100 (2%) EIA neg. samples were reactive and 95/100 (95%) were non-reactive by both assays. Three (3%) were only HCV Qual (TMA) reactive, while 11/14 TMA+/PCR-samples with sufficient volume were genotyped. The authors concluded that HCV Qual (TMA) identified active HCV infection in more EIA pos. and EIA neg. patients than HCV Qual (PCR) and should be part of their testing algorithm.
IT **735853-91-5**
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(HCV-specific nested PCR primer; comparison of hemodialysis patients using transcription mediated amplification-based VERSANT HCV RNA Qual. Assay and inhouse PCR for detection of hepatitis C virus in hemodialysis patients)
REFERENCE COUNT: 56 THERE ARE 56 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 9 OF 46 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2005:128021 CAPLUS
DOCUMENT NUMBER: 142:458047
TITLE: Amplifying nucleic acid by linear and circular oligonucleotides
INVENTOR(S): Tian, Jingdong; Gong, Qihong
PATENT ASSIGNEE(S): Peop. Rep. China
SOURCE: Faming Zhuanli Shenqing Gongkai Shuomingshu, 31 pp.
CODEN: CNXXEV
DOCUMENT TYPE: Patent
LANGUAGE: Chinese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
CN 1460722	A	20031210	CN 2003-123596	20030519
PRIORITY APPLN. INFO.:			CN 2003-123596	20030519

ED Entered STN: 15 Feb 2005
AB The current invention provides a method for amplifying nucleic acid by linear and circular oligonucleotides. The method consists of more than one pair of linear probe and circular probe (ratio 1-100 to 1-100 mol/mol). The linear probe consists of a test nucleic acid sequence matching the target 5' end (15-35 mer), a circular probe matching its 3' end (2-10 mer), and a spacer (0-5 mer). The circular probe consists of a test nucleic acid sequence matching sequence (15-35 mer), a linear probe

3' end-matching sequence (2-10 mer), and a spacer (0-5 mer). The linear probe may be fixed partly or completely on a carrier. A linear primer may be added in each pair of the linear probe and circular probe. Examples for detecting hepatitis C virus RNA and human cytomegalovirus DNA are given.

IT 851551-43-4, 1: PN: CN1460722 SEQID: 1 claimed RNA
851551-44-5, 2: PN: CN1460722 SEQID: 2 claimed DNA
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(oligonucleotide probe; amplifying nucleic acid by linear and circular oligonucleotides)

L7 ANSWER 10 OF 46 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2003:311822 CAPLUS
DOCUMENT NUMBER: 139:144477
TITLE: Determination of hepatitis C virus genotype by Pyrosequencing
AUTHOR(S): Elahi, Elahe; Pourmand, Nader; Chaung, Ramsey; Rofoogaran, Ara; Boisver, Judie; Samimi-Rad, Katayon; Davis, Ronald W.; Ronaghi, Mostafa
CORPORATE SOURCE: Stanford Genome Technology Center, Stanford University, Palo Alto, CA, 94304, USA
SOURCE: Journal of Virological Methods (2003), 109(2), 171-176
CODEN: JVMEDH; ISSN: 0166-0934
PUBLISHER: Elsevier Science B.V.
DOCUMENT TYPE: Journal
LANGUAGE: English
ED Entered STN: 23 Apr 2003
AB A simple sequencing-based assay is described for genotyping of hepatitis C virus (HCV). RT-PCR was employed to amplify a 237-nucleotide-long fragment from the 5' untranslated region (UTR) of the genome using one biotinylated and one normal primer. Subsequent to capture of the PCR products on streptavidin-coated beads, single-stranded DNA separation, and hybridization of sequencing primer, Pyrosequencing was performed. The genotype of 98 samples out of which 77 samples were from American veterans and 21 samples were from Iran was determined The samples from the American veterans contained six different subtypes, while five subtypes were found in Iranian samples. For rapid population-specific HCV subtyping, a multiplex assay was developed. This study demonstrates the suitability of this technol. for low-cost, high throughput and accurate microbial genotyping.

IT 569477-14-1
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(PCR primer for HCV 5'-UTR; hepatitis C virus genotype by Pyrosequencing)

REFERENCE COUNT: 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 11 OF 46 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2002:754625 CAPLUS
DOCUMENT NUMBER: 137:274028
TITLE: Probes and SNP in human protein MxA and mannose binding lectin gene for diagnosis of hepatitis C
INVENTOR(S): Hashimoto, Koji; Hashimoto, Michie; Mishiro, Shunji; Oota, Yasuhiko
PATENT ASSIGNEE(S): Kabushiki Kaisha Toshiba, Japan
SOURCE: PCT Int. Appl., 125 pp.
CODEN: PIXXD2

DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002077281	A1	20021003	WO 2002-JP2030	20020305
W: CN, KR, RU, US				
RW: DE, ES, FR, GB, GR, IT, SE				
JP 2003088382	A2	20030325	JP 2001-284112	20010918
EP 1375672	A1	20040102	EP 2002-702736	20020305
R: DE, ES, FR, GB, GR, IT, SE				
RU 2229719	C2	20040527	RU 2002-106731	20020305
JP 2002355083	A2	20021210	JP 2002-86681	20020326
US 2004043379	A1	20040304	US 2003-70415	20030129
JP 2005341974	A2	20051215	JP 2005-239873	20050822
PRIORITY APPLN. INFO.:			JP 2001-90053 A	20010327
			JP 2001-284112 A	20010918
			WO 2002-JP2030 W	20020305

ED Entered STN: 04 Oct 2002
AB This invention provides a method of diagnosis of hepatitis C. Probes specific to hepatitis C virus were provided in this invention for diagnosis of hepatitis C. The invention also provides probes for identification of SNP in human protein MxA gene promoter region and in mannose binding lectin gene. The sequences of probes specific to hepatitis C virus and allele variant of MxA and MBL genes were disclosed. Interferon treatment was effective on the hepatitis C patient with SNP in MxA and MBL genes.
IT **465577-45-1**
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(nucleic acid sequence; probes and SNP in human protein MxA and mannose binding lectin gene for diagnosis of hepatitis C)
REFERENCE COUNT: 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 12 OF 46 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2002:504958 CAPLUS
DOCUMENT NUMBER: 137:74395
TITLE: Oligonucleotide probes and primers for detecting pathogenic microorganism
INVENTOR(S): Shimada, Masamitsu; Hino, Fumitsugu; Kato, Ikunoshin
PATENT ASSIGNEE(S): Takara Shuzo Co., Ltd., Japan
SOURCE: PCT Int. Appl., 106 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 4
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002052043	A1	20020704	WO 2001-JP111422	20011226
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA,				

UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

EP 1347060	A1	20030924	EP 2001-272324		20011226
CN 1491285	A	20040421	CN 2001-822774		20011226
US 2004185455	A1	20040923	US 2003-451882		20030626
PRIORITY APPLN. INFO.:			JP 2000-396222	A	20001226
			JP 2000-396321	A	20001226
			JP 2001-199552	A	20010629
			JP 2001-278920	A	20010913
			WO 2001-JP11422	W	20011226

ED Entered STN: 05 Jul 2002

AB A method and kits containing oligonucleotide probes and primers for detecting pathogenic microorganisms. The probes and primers target IS6110 gene of Mycobacterium tuberculosis, Neisseria gonorrhoeae cppB gene, Chlamydia trachomatis cryptic plasmid pLGV440, and hepatitis C virus (HCV) 5'-UTR. The probes may be labeled with a fluorophore and quencher for FRET, chromophore, enzyme, biotin, gold colloid, and radioisotope. The kit contains DNA polymerase with strand displacement capability, RNaseH, deoxyribonucleotide triphosphates. Bca DNA polymerase lacking 5'-3' exonuclease from Bacillus caldotenax and RNaseH from Pyrococcus or Archaeoglobus may be used preferably. Microtiter plate, beads, magnetic beads, membrane, or glass are used as substrate for capturing amplified fragments. Chimeric oligonucleotide primers may be used for nucleic acid amplification. Use of FITC or TAMRA labeled probes are described.

IT 440077-63-4
RL: PRP (Properties)
(unclaimed nucleotide sequence; oligonucleotide probes and primers for detecting pathogenic microorganism)

REFERENCE COUNT: 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 13 OF 46 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2002:504956 CAPLUS
DOCUMENT NUMBER: 137:74394
TITLE: Method of generating an improved internal control for diagnosis of viral infections using a 5' nuclease PCR assay
INVENTOR(S): Gessner, Matthias
PATENT ASSIGNEE(S): Baxter Aktiengesellschaft, Austria
SOURCE: PCT Int. Appl., 37 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002052041	A2	20020704	WO 2001-EP15069	20011219
WO 2002052041	A3	20040219		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW

102(a) date

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

US 2002137039 A1 20020926 US 2000-746874 20001222

PRIORITY APPLN. INFO.: US 2000-746874 A 20001222

ED Entered STN: 05 Jul 2002

AB Nucleic acid amplification assays using a 5' nuclease and having internal amplification controls are provided. Related methods for preparing the internal controls are also provided. Moreover, methods for rapidly and accurately determining optimum nucleic acid sequences for the internal amplification controls of the 5' nuclease assays are provided. The method involves constructing an internal control oligonucleotide comprising an inverted target oligonucleotide probe binding site and an internal control probe with a nucleic acid sequence complementary to the inverted target oligonucleotide probe binding site. Thus, the internal control probe hybridizes with the internal control oligonucleotide when sequences are complementary and hybridization results in degradation of detectably labeled probes by the nuclease activity of polymerase in PCR reaction. Both the internal control probe and the internal control oligonucleotide are amplified by the same primers. The 5' nuclease PCR assay may be used for the detection of pathogens. In a preferred embodiment, hepatitis C virus detection is performed using a 5' nuclease PCR assay.

IT **439889-66-4**

RL: PRP (Properties)
(unclaimed nucleotide sequence; method of generating an improved internal control for diagnosis of viral infections using a 5' nuclease PCR assay)

L7 ANSWER 14 OF 46 CAPLUS COPYRIGHT 2006 ACS on STN

ACCESSION NUMBER: 2002:185367 CAPLUS

DOCUMENT NUMBER: 136:242902

TITLE: A multiplex primer extension method of DNA fingerprinting for rapid identification

INVENTOR(S): Ronaghi, Mostafa; Ekstroem, Bjoern; Pourmand, Nader

PATENT ASSIGNEE(S): Pyrosequencing AB, Swed.; The Board of Trustees of the Leland Stanford Junior University; Gardner, Rebecca

SOURCE: PCT Int. Appl., 86 pp.
CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002020837	A2	20020314	WO 2001-GB4042	20010910
WO 2002020837	A3	20030313		

W: AE, AG, AL, AM, AT, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, CZ, DE, DE, DK, DK, DM, DZ, EC, EE, EE, ES, FI, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

CA 2421857	AA	20020314	CA 2001-2421857	20010910
AU 2001084308	A5	20020322	AU 2001-84308	20010910

EP 1322782	A2	20030702	EP 2001-963280		20010910
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR					
JP 2004508055	T2	20040318	JP 2002-525843		20010910
US 2005084851	A1	20050421	US 2003-363177		20010910
PRIORITY APPLN. INFO.:			GB 2000-22069	A	20000908
			WO 2001-GB4042	W	20010910

ED Entered STN: 15 Mar 2002

AB A rapid method of fingerprinting DNA using a derivative of multiplex PCR is described. The method involves using several pairs of primers that within a limited target region of the DNA of interest. Individual nucleotides are added to the reaction one at a time in a fixed order. By measuring the incorporation of the added nucleotides into the primer extension products, a fingerprint of the DNA sequence is derived. Unincorporated nucleotides from each round of the addition are degraded with an enzyme such as a nucleoside triphosphatase. Use of the method to identify hepatitis C virus in blood samples and in the anal. of single nucleotide polymorphisms is demonstrated.

IT 404321-95-5
RL: PRP (Properties)
(unclaimed nucleotide sequence; multiplex primer extension method of DNA fingerprinting for rapid identification)

L7 ANSWER 15 OF 46 CAPLUS COPYRIGHT 2006 ACS on STN

ACCESSION NUMBER: 2002:90251 CAPLUS
DOCUMENT NUMBER: 136:146152
TITLE: Nucleic acid construct and methods for detecting RNA viral infection, screening for anti-viral drug and determining drug resistance of isolated virus
INVENTOR(S): Tan, Yin Hwee; Lim, Siew Pheng; Lim, Seng Gee; Hong, Wan Jin
PATENT ASSIGNEE(S): Institute of Molecular & Cell Biology, Singapore; Ehrlich, Gal
SOURCE: PCT Int. Appl., 81 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

(a)

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002008447	A2	20020131	WO 2001-IL669	20010720
WO 2002008447	A3	20031030		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
AU 2001082417	A5	20020205	AU 2001-82417	20010720
EP 1373576	A2	20040102	EP 2001-961035	20010720
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI, CY, TR				
US 2004137424	A1	20040715	US 2003-333449	20030804
PRIORITY APPLN. INFO.:			US 2000-220248P	P 20000724

possible (e) date

WO 2001-IL669 W 20010720

ED Entered STN: 01 Feb 2002

AB The present invention relates to nucleic acid constructs and methods of utilizing same for detecting infection of an RNA virus, for uncovering anti-viral drug candidates and for determining drug resistance of isolates of an RNA virus. More particularly, the present invention relates to a nucleic acid construct which transcribes a minus strand RNA sequence encoding a reporter polypeptide and including 5' and 3' sequences of an RNA virus. When transcribed in a cell infected with an RNA virus capable of replicating the minus strand RNA sequence, a plus strand of this RNA sequence is formed and translated by the host cell into an active reporter polypeptide. Sequences of complete HCV genome were generated and incorporated in novel chimeric HCV-luciferase expression constructs which can be used in accurate and rapid cell based assays for detecting HCV infection, screening mols. for potential anti-viral activities and determining drug resistance of HCV isolates. The invention demonstrated that neg. strand synthesis depends on expression of essentially all the viral proteins in intact cells. Based on these findings, the present invention provides a cell-based HCV replication-dependent system that is a measure of the activity of the full-length HCV genome. This system is simple, and robust and highly reproducible and in addition, enables to measure viral activity as early as three days post-transfection.

IT **393599-90-1**
RL: PRP (Properties)
(unclaimed nucleotide sequence; nucleic acid construct and methods for detecting RNA viral infection, screening for anti-viral drug and determining drug resistance of isolated virus)

L7 ANSWER 16 OF 46 CAPLUS COPYRIGHT 2006 ACS on STN

ACCESSION NUMBER: 2003:248483 CAPLUS
DOCUMENT NUMBER: 140:71641
TITLE: Genotyping of hepatitis C virus by hepatitis gene diagnosis microarray
AUTHOR(S): Zhao, Wei; Liu, Wei; Liu, Quanjun; Zhang, Lin; Zhou, Zhenxian; Liu, Xinjue; Zhang, Hanrong
CORPORATE SOURCE: Department of Pathology, Nanjing Second Hospital Affiliated to Medical College of Southeast University, Nanjing, 210003, Peop. Rep. China
SOURCE: Zhonghua Yixue Zazhi (Beijing, China) (2002), 82(18), 1249-1253
CODEN: CHHTAT; ISSN: 0376-2491
PUBLISHER: Zhonghua Yixue Zazhishe
DOCUMENT TYPE: Journal
LANGUAGE: Chinese

ED Entered STN: 01 Apr 2003

AB The preparation of hepatitis C virus (HCV) diagnosis microarray and its accuracy in diagnosis of genotype of hepatitis C virus were studied. Probes and primers were designed based on 5'-untranslated region and C region of hepatitis C virus gene. The probes were synthesized by DNA synthesizer. Solns. of probe of the final concentration of 50 μmol/L were made by dissolving the probes into sodium carbonate buffer. Hepatitis C virus genotype array spotting was performed by pin-based spotting robot PixSys5500 with CMP3 pin. The gene chips were prepared by spotting the probes onto the specially treated glass sliders. Sixty HCV RNA pos. serum samples were obtained from the in-patients of the Nanjing Second Hospital(exptl. group), and 60 HCV RNA neg. serum samples were obtained from the healthy people undergoing phys. examination(control group). Quant. examination of serum HCV RNA was made by fluorescent quantitation PCR. The HCV RNA in the serum specimens of the exptl. group and of the control group

(with the HCV RNA concentration of less than 500 copies/mL) was isolated and purified, underwent reversed transcription and nested PCR to be amplified, and then genotyped by gene microarray and HCV RNA sequencing. During the experiment, double blind method was used. Tested by the gene microarray, the serum specimens in the exptl. group were all HCV RNA pos., out of which 46 cases were 1b type, 3 cases were 3a type, 3 cases were 3b type, 2 cases were 2a type, 2 cases were 2b type, 2 cases were 1b + 2a type, and 2 cases were 3a type. Tested by nucleotide sequencing assay, 50 cases were 1b type, 3 cases were 3a type, 3 cases were 3b type, 2 cases were 2a type, and 2 cases were 2b type. The double-blind test results showed a coincidence rate of 93.3% in genotyping HCV by these two methods. Hepatitis gene microarray can be used in detection of serum HCV RNA and in diagnostic genotyping with great accuracy.

IT **639866-21-0**
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(primer sequence; genotyping of hepatitis C virus by diagnosis microarray using probes designed from 5'-untranslated region and C region of hepatitis C virus gene)

L7 ANSWER 17 OF 46 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2002:134009 CAPLUS
DOCUMENT NUMBER: 137:333595
TITLE: Two-round rapid-cycle RT-PCR in single closed capillaries increases the sensitivity of HCV RNA detection and avoids amplicon carry-over
AUTHOR(S): Ratge, D.; Scheiblhuber, B.; Landt, O.; Berg, J.; Knabbe, C.
CORPORATE SOURCE: Institute of Clinical Pathology, Robert Bosch Hospital, Stuttgart, D-70376, Germany
SOURCE: Journal of Clinical Virology (2002), 24(3), 161-172
CODEN: JCVIFB; ISSN: 1386-6532
PUBLISHER: Elsevier Science Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English
ED Entered STN: 20 Feb 2002
AB For the detection of hepatitis C virus (HCV) specific nucleic acids the polymerase chain reaction (PCR) is widely used. Rapid-cycle PCR is performed in glass capillaries with the LightCycler instrument and allows PCR including product anal. to be performed within a closed system in about 1 h. Thus, rapid-cycle PCR appears especially suitable for routine diagnostic applications. However, the volume of the PCR vessel is restricted to about 20 μl, which may limit the sensitivity of the PCR. To increase its sensitivity two-round or nested primer PCR protocols have been developed. In rapid-cycle PCR first-round PCR products are usually collected from the capillaries by centrifugation, a procedure prone to cross-contamination. The objective was development of a two-round rapid-cycle reverse transcription-polymerase chain reaction (RT-PCR) in single closed LightCycler capillaries for the sensitive detection of HCV RNA in serum or plasma. A set of two pairs of nested primers was selected. The first-round RT-PCR reaction mixture was separated from the second-round PCR mixture by silicone oil. Reverse transcription followed by the first-round PCR was performed. Then, the second-round mixture was combined with first-round products by a centrifugation step followed by second round PCR during which fluorescence intensities were recorded and used for quantification. To establish the sensitivity of this novel assay a serial dilution of HCV reference standard was used. In plasma samples about 100
IU/mL HCV were consistently detected using the high pure viral RNA kit for nucleic acid purification This detection limit was found to be about 20 fold

increased compared with single-round RT-PCR and corresponded to 3.4 IU of HCV per capillary. Using a panel of HCV genotype stds. the novel assay exhibited similar sensitivity for all HCV genotypes. The applicability for clin. routine testing was demonstrated by examining 156 clin. samples. Two-round RT-PCR with the LightCycler instrument using a single closed capillary throughout the procedure was found ideally suited for rapid (100 min), accurate and sensitive mol. diagnosis of active HCV infections. Since the capillaries remained closed during the procedure carry-over contamination was precluded.

IT **473858-57-0**
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(hepatitis C virus specific PCR primer ncl; two-round rapid-cycle RT-PCR in single closed capillaries increases the sensitivity of hepatitis C virus (HCV) RNA detection and avoids amplicon carry-over)

REFERENCE COUNT: 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 18 OF 46 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2002:151355 CAPLUS
DOCUMENT NUMBER: 137:227055
TITLE: Real-time RT-PCR for quantitation of hepatitis C.virus RNA
AUTHOR(S): Yang, Ji-Hong; Lai, Jian-Ping; Douglas, Steven D.; Metzger, David; Zhu, Xian-Hua; Ho, Wen-Zhe
CORPORATE SOURCE: Division of Immunologic and Infectious Diseases, Joseph Stokes Jr. Research Institute, Children's Hospital of Philadelphia, Philadelphia, PA, 19104, USA
SOURCE: Journal of Virological Methods (2002), 102(1-2), 119-128
CODEN: JVMEDH; ISSN: 0166-0934
PUBLISHER: Elsevier Science B.V.
DOCUMENT TYPE: Journal
LANGUAGE: English
ED Entered STN: 27 Feb 2002
AB A newly developed real-time RT-polymerase chain reaction assay for quantitation of hepatitis C virus (HCV) RNA in human plasma and serum was applied. A pair of primers and a probe (mol. beacon) were designed that are specific for the recognition of a highly conservative 5'-non-coding region (5'-NCR) in HCV genome. HCV real-time RT-PCR assay had a sensitivity of 1000 RNA copies per reaction, with a dynamic range of detection between 103 and 107 RNA copies. The coefficient variation of threshold cycle (Ct) values in intra- and inter-runs were less than 1.37 and 4.66%, resp. The real-time RT-PCR assay on the HCV sero-pos. samples yielded reproducible data, with less than 2.09% of the inter-assay variation. In order to determine its potential for clin. diagnosis, real-time RT-PCR was used to examine the HCV RNA levels in plasma from sero-pos. and neg. subjects, showing that the assay is highly sensitive and has specificity of 100%. It was demonstrated that the real-time RT-PCR was able to amplify HCV RNA in reference sera with seven genotypes (1A, 1B, 2B, 3A, 4, 5A and 6A) that include six major HCV genotypes circulated in the world. Since HCV is a major pathogen of post-transfusion and community-transmitted non-A, non-B hepatitis, this assay has a broad application for basic and clin. investigations.

IT **459459-16-6**
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(PCR primer; real-time RT-PCR for quantitation of hepatitis C virus RNA)

REFERENCE COUNT: 35 THERE ARE 35 CITED REFERENCES AVAILABLE FOR THIS

RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 19 OF 46 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2001:380605 CAPLUS
DOCUMENT NUMBER: 135:15051
TITLE: Simultaneous detection of HBV, HCV and HIV in plasma samples using a multiplex capture assay by PCR and RT-PCR
INVENTOR(S): Ji, Jiuping; Manak, Mark; Wu, Kezuo; Chen, Xiuli; Yang, Lijuan
PATENT ASSIGNEE(S): USA
SOURCE: PCT Int. Appl., 51 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001036442	A1	20010525	WO 2000-US31738	20001117
WO 2001036442	C2	20020725		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
CA 2392218	AA	20010525	CA 2000-2392218	20001117
EP 1233976	A1	20020828	EP 2000-980521	20001117
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR				
US 2004072148	A1	20040415	US 2003-407897	20030407

PRIORITY APPLN. INFO.: US 1999-165916P P 19991117
WO 2000-US31738 W 20001117

ED Entered STN: 27 May 2001
AB The present invention is directed to a capture assay to simultaneously screen for HBV, HCV and HIV nucleic acids in samples such as plasma. The nucleic acids including both viral DNA and RNA are purified from the plasma samples in a single extraction procedure. In one embodiment, a mixture of degenerate biotin-labeled PCR primers specific for the HBV, HCV, HIV-1 type M and HIV-1 type O are used to amplify any of these viruses which may be present in plasma. Amplified products are captured by hybridization to immobilized capture sequence, and thereafter detected. An internal control vector containing a synthetic fragment flanked by sequences corresponding to the HBV primers was designed to monitor sample recovery during extraction, amplification and detection. All major subtypes of HBV, HCV and HIV-1 including HIV-1 type O have been confirmed and detected by the assay.
IT 157607-57-3
RL: PRP (Properties)
(unclaimed sequence; simultaneous detection of HBV, HCV and HIV in plasma samples using a multiplex capture assay by PCR and RT-PCR)
REFERENCE COUNT: 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 20 OF 46 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2000:133881 CAPLUS
DOCUMENT NUMBER: 132:176578
TITLE: Primer-specific and mispair extension assay (PSMEA) genotyping system for identifying gene variation
INVENTOR(S): Hu, Yu-wen
PATENT ASSIGNEE(S): Canadian Blood Services, Can.; Hema-Quebec
SOURCE: PCT Int. Appl., 65 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000009745	A1	20000224	WO 1999-CA733	19990809
W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
CA 2245039	AA	20000213	CA 1998-2245039	19980813
CA 2339323	AA	20000224	CA 1999-2339323	19990809
AU 9952728	A1	20000306	AU 1999-52728	19990809
US 2002064778	A1	20020530	US 2001-782361	20010213
US 6811974	B2	20041102		

PRIORITY APPLN. INFO.:			
	CA 1998-2245039	A	19980813
	WO 1999-CA733	W	19990809

ED Entered STN: 25 Feb 2000
AB The invention presents a novel genotyping system, primer specific and mispair extension assay (PSMEA), to detect nucleotide variations in any known gene sequence using Pfu DNA polymerase in the presence of an incomplete set of radioactively labeled dNTPs and only a single labeled primer. The PSMEA assay comprises: (a) extending a DNA sequence amplified from a patient sample with pfu DNA polymerase using a genotype-specific primer and an incomplete set of dNTPs, under suitable conditions for obtaining extension of the primer; (b) separating the extended DNA sequences obtained in step (a); (c) detecting the separated DNA sequences and (d) comparing the extended DNA sequences with known DNA sequences for various genotypes for determining the genotype of the extended DNA sequence. To test the feasibility of PSMEA, the 5'-untranslated region (5'-UTR) of the hepatitis C virus genome was used in the invention as a model for anal. of nucleotide variation in determining the type and subtype of the virus. The invention also demonstrated the use of the PSMEA for detection of low levels of drug resistant HIV-1 mutants in patients being treated with antiviral drugs (reverse transcriptase and protease inhibitors). The PSMEA is based on the unique 3'-5'-proofreading activity of pfu DNA polymerase in a reaction with an incomplete set of dNTPs. The invention also included primers able to amplify the 5'-UTR of the hepatitis C virus genome and the reverse transcriptase and protease genes of HIV-1 mutants.
IT **259204-93-8**
RL: ARG (Analytical reagent use); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(sense universal PCR primer (first round); primer-specific and mispair extension assay (PSMEA) used for genotyping hepatitis C virus)

REFERENCE COUNT: 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 21 OF 46 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2000:12729 CAPLUS
DOCUMENT NUMBER: 132:74503
TITLE: An isothermal amplification method for the detection of a specific RNA
INVENTOR(S): Ishiguro, Takahiko; Saitoh, Juichi; Ishizuka, Tetsuya
PATENT ASSIGNEE(S): Tosoh Corp., Japan
SOURCE: Eur. Pat. Appl., 39 pp.
CODEN: EPXXDW
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 969101	A1	20000105	EP 1999-112731	19990701
EP 969101	B1	20040331		
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
JP 2000014400	A2	20000118	JP 1998-186434	19980701
US 2001053518	A1	20011220	US 1999-345761	19990701
US 2004115718	A1	20040617	US 2003-687588	20031020
PRIORITY APPLN. INFO.:			JP 1998-186434 A	19980701
			US 1999-345761 B1	19990701

ED Entered STN: 06 Jan 2000
AB A method of detecting a specific RNA in a population by specific isothermal amplification without the need to fractionate the amplification products is described. The RNA is first trimmed to create a defined 5'-end using a combination of RNase H and an oligodeoxyribonucleotide probe and this is then converted to a full-length RNA/cDNA hybrid using reverse transcriptase. The sample is then made 5-20 volume% in DMSO and a pair of primers with one carrying a promoter are then used to convert the cDNA to double stranded DNA that is then transcribed to amplify the target sequence. The transcription products are then detected with a specific probe that is labeled with an intercalating dye so that binding of the probe to the target leads to an increase in fluorescence.
IT 253656-91-6
RL: PRP (Properties)
(unclaimed nucleotide sequence; isothermal amplification method for the detection of a specific RNA)
REFERENCE COUNT: 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 22 OF 46 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 1999:375699 CAPLUS
DOCUMENT NUMBER: 131:41800
TITLE: Sensitive, high-throughput screening of blood by hybridization and immunoassay without amplification of analyte sequences
INVENTOR(S): Primi, Daniele; Mantero, Giovanni
PATENT ASSIGNEE(S): Diasorin International Inc., USA
SOURCE: PCT Int. Appl., 73 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9928503	A1	19990610	WO 1998-US24494	19981116
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
CA 2312192	AA	19990610	CA 1998-2312192	19981116
AU 9915265	A1	19990616	AU 1999-15265	19981116
EP 1034303	A1	20000913	EP 1998-959477	19981116
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				

PRIORITY APPLN. INFO.: IT 1997-RM749 A 19971203
WO 1998-US24494 W 19981116

ED Entered STN: 17 Jun 1999

AB Sensitive and specific methods of detecting single-stranded polynucleotide analytes can be used in manual or automated diagnostic assays and to screen blood samples for the presence of infectious agents. The methods can be used to detect any single-stranded polynucleotide analyte whose sequence is known. Single-stranded DNA analytes which are present in a biol. sample at a concentration of 0.1 fg/μl can be detected. This sensitivity can be achieved using linear, rather than exponential, amplification of the target sequence. The method uses an immobilized single-stranded probe to capture a single-stranded target sequence and the formation of the immobilized double-stranded hybrid is measured using a monoclonal antibody from the autoimmune MRL/lpr mouse to double-stranded nucleic acids. RNA viruses can be detected after conversion of viral nucleic acids to cDNA.

IT **227013-13-0**
RL: ARG (Analytical reagent use); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(primer for linear amplification of hepatitis C virus DNA; sensitive, high-throughput screening of blood by hybridization and immunoassay without amplification of analyte sequences)

REFERENCE COUNT: 12 THERE ARE 12 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 23 OF 46 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 1996:640853 CAPLUS
DOCUMENT NUMBER: 125:294151
TITLE: Comparative analysis of three nucleic acid-based detection systems for hepatitis C virus RNA in plasma from liver transplant recipients
AUTHOR(S): Chen, Yiping; Cooper, David L.; Ehrlich, Garth D.
CORPORATE SOURCE: Dep. Pathology, Univ. Pittsburgh, Pittsburgh, PA, 15261, USA
SOURCE: Molecular and Cellular Probes (1996), 10(5), 331-336
CODEN: MCPRE6; ISSN: 0890-8508
PUBLISHER: Academic
DOCUMENT TYPE: Journal
LANGUAGE: English

ED Entered STN: 30 Oct 1996

AB The early detection of hepatitis C viremia (HCV) following liver transplantation is important for monitoring disease recurrence and

planning antiviral chemotherapy. In the current study, the sensitivity, specificity, and concordance of three HCV RNA assays were compared using a random sample of 84 plasma specimens from 23 transplant recipients. Two of the assays were prototype com. tests: Roche Mol. Diagnostic's RT-PCR HCV AmplicorTM system; and Chiron's QuantiplexTM HCV-RNA assay. The third was a 'home brew' PCR-liquid hybridization/gel retardation assay developed at the University of Pittsburgh Medical Center (UPMC). On all criteria the PCR-based assays out-performed the Quantiplex assay and displayed an overall concordance of 87%. A high percentage of specimens in the Quantiplex assay gave indeterminate results (12%) or high coeffs. of variance (13%). The specificities of all RNA assays were determined using HCV serostatus as the gold standard Both of the PCR-based assays had specificities of 100%, whereas the Chiron Quantiplex HCV assay had a specificity of 88%, if indeterminates were counted as sensitivities of the PCR-based assays were 56% and 48% for the 'home brew' and the Roche assays, resp. The UPMC HCV assay, however, was determined to be capable of reproducibly detecting four or fewer chimpanzee infectious doses, suggesting that HCV viremia was not present in the PCR-neg. cases. The sensitivity of the Quantiplex assay was 41% counting indeterminates as negatives and 46% counting them as positives. The high cost of the Quantiplex assay combined with the number of uninterpretable results, the lack of sensitivity, and reduced specificity may limit the usefulness of this assay for monitoring HCV recurrence.

IT 182895-29-0
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses) (primer HCV101; comparative anal. of three nucleic acid-based detection systems for hepatitis C virus RNA in plasma from liver transplant recipients)

L7 ANSWER 24 OF 46 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 1995:847767 CAPLUS
DOCUMENT NUMBER: 124:22843
TITLE: Hepatitis C virus genotyping by means of 5'-UR/core line probe assays and molecular analysis of untypeable samples
AUTHOR(S): Stuyver, Lieven; Wyseur, Ann; van Arnhem, Wouter; Lunel, Francoise; Laurent-Puig, Pierre; Pawlotsky, Jean-Michel; Kleter, Bernhard; Bassit, Leda; Nkengasong, John; et al.
CORPORATE SOURCE: Innogenetics N.V., Industriepark 7, Box 4, Ghent, B-9052, Belg.
SOURCE: Virus Research (1995), 38(2-3), 137-57
CODEN: VIREDF; ISSN: 0168-1702
PUBLISHER: Elsevier
DOCUMENT TYPE: Journal
LANGUAGE: English
ED Entered STN: 11 Oct 1995
AB To test the theor. possibility of 5'-UR mistyping between hepatitis C virus subtypes 1a and 1b, a 5'-UR/Core line probe assay (LiPA) was combined with a nested PCR system and 183 sera were retested that had been previously genotyped as type 1a or 1b and originating mainly from Western Europe. Eight percent of these were found to be wrongly subtyped. Based on this method, 3 addnl. subtypes of type 1 were discovered (1d-1f). Randomly selected European type 2 sera were tested with a similar type 2 5'-UR/Core LiPA. They were unexpectedly found to belong to subtype 2c in the majority of cases. Among serum samples originating from SouthEast Asia, several addnl. genotypes (7a, 7c, 7d, and 9a) were detected which had 5'-UR sequence motifs indistinguishable from genotype 1. Based on 13,203 pairwise comparisons in the 340-bp NS5B region, classification into types, subtypes, and isolates was obtained in 99.8% of all cases by using

*

On support?
no - it's in a primer
see p. 143

the phylogenetic border value of 0.328 for subtypes/types and 0.127 for isolates/subtypes; and evidence for a 10th major type of HCV was provided. Combination of all available HCV sequence data from the 447-bp Core/E1 region and the NS5B 340-bp and 222-bp regions provided evidence for the existence of 10 types, including 50 subtypes. Previously, extensive studies involving genotypes 1a, 1b, 2a, and 2b indicated the importance of HCV subtyping in interferon treatment and progression of chronic liver disease. The herein described expansion in the number of HCV types and subtypes should help improve diagnosis, treatment, and possibly prophylaxis of hepatitis C liver disease.

IT **171761-22-1**
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses) (PCR primer; hepatitis C virus genotyping by 5'-UR/core line probe assays and mol. anal. of untypeable samples)

L7 ANSWER 25 OF 46 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 1994:572244 CAPLUS
DOCUMENT NUMBER: 121:172244
TITLE: Typing of isolates of hepatitis C virus isolates with a panel of probes directed against an untranslated region of the viral genome
INVENTOR(S): Maertens, Geert; Stuyver, Lieven; Rossau, Rudi; Van Heuverswyn, Hugo
PATENT ASSIGNEE(S): Belg.
SOURCE: PCT Int. Appl., 95 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9412670	A2	19940609	WO 1993-EP3325	19931126
WO 9412670	A3	19940721		
W: AT, AU, BB, BG, BR, BY, CA, CH, CZ, DE, DK, ES, FI, GB, HU, JP, KP, KR, KZ, LK, LU, LV, MG, MN, MW, NL, NO, NZ, PL, PT, RO, RU, SD, SE, SK, UA, US, UZ, VN				
RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
CA 2128528	AA	19940609	CA 1993-2128528	19931126
AU 9456282	A1	19940622	AU 1994-56282	19931126
AU 681612	B2	19970904		
EP 637342	A1	19950208	EP 1994-901891	19931126
EP 637342	B1	19990428		
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE				
JP 07503143	T2	19950406	JP 1994-512767	19931126
EP 905258	A2	19990331	EP 1998-117538	19931126
EP 905258	A3	20010131		
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE				
AT 179459	E	19990515	AT 1994-901891	19931126
ES 2133529	T3	19990916	ES 1994-901891	19931126
EP 1197568	A2	20020417	EP 2001-121347	19931126
EP 1197568	A3	20040414		
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE				
US 5846704	A	19981208	US 1994-256568	19940718
US 6171784	B1	20010109	US 1998-38369	19980310
US 6051696	A	20000418	US 1998-44665	19980319
US 6495670	B1	20021217	US 1999-378900	19990823
US 2002106638	A1	20020808	US 2001-899082	20010706

US 6891026	B2	20050510		
US 2002168626	A1	20021114	US 2001-899302	20010706
US 6887985	B2	20050503		
US 2003036053	A1	20030220	US 2001-899044	20010706
US 6548244	B2	20030415		
US 2004191768	A1	20040930	US 2004-822711	20040413
JP 2005040145	A2	20050217	JP 2004-328242	20041111

PRIORITY APPLN. INFO.:

EP 1992-403222	A 19921127
EP 1993-402129	A 19930831
EP 1994-901891	A3 19931126
EP 1998-117538	A3 19931126
JP 1994-512767	A3 19931126
WO 1993-EP3325	W 19931126
US 1994-256568	A3 19940718
US 1998-44665	A3 19980319
US 1999-378900	A3 19990823
US 2001-899082	A3 20010706

ED Entered STN: 15 Oct 1994

AB A process for genotyping any HCV isolate in a biol. sample and for classifying said isolate according to its homol. with other HCV isolates uses a panel of hybridization probes against a domain extending from nucleotide at position -291 to nucleotide at position -66 of the 5' untranslated region of one of the HCV isolates represented by their cDNA sequences. Primers for amplification of the untranslated region prior to hybridization are also described. Patterns of hybridization for identifying specific types are reported.

IT (157607-57-3)
RL: USES (Uses)
(PCR primer for amplification of 5'-untranslated region of hepatitis C virus RNA, typing of virus by hybridization in relation to)

L7 ANSWER 26 OF 46 CAPLUS COPYRIGHT 2006 ACS on STN

ACCESSION NUMBER: 1995:257984 CAPLUS
DOCUMENT NUMBER: 122:48482
TITLE: Method and PCR primer set for hepatitis C virus grouping
INVENTOR(S): Hasegawa, Akira; Yamaguchi, Kenjiro
PATENT ASSIGNEE(S): Tonen Corp, Japan
SOURCE: Jpn. Kokai Tokkyo Koho, 8 pp.
CODEN: JKXXAF
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
JP 06292600	A2	19941021	JP 1993-83289	19930409

PRIORITY APPLN. INFO.: JP 1993-83289 19930409

ED Entered STN: 22 Dec 1994

AB Disclosed is a PCR method with two sense primers for diagnosing and grouping hepatitis C virus. The grouping can improve the effectiveness of interferon therapy, since interferon is only effective for group II hepatitis C. In example, total RNA was extracted from hepatitis C virus, cDNA was prepared by PCR, PCR-SSCP (single standard conformation polymorphism) method was performed, and the relationship between effective interferon therapy and hepatitis C virus grouping was compared.

IT (159942-56-0)
RL: ARG (Analytical reagent use); THU (Therapeutic use); ANST (Analytical

study); BIOL (Biological study); USES (Uses)
(PCR primer set for hepatitis C virus grouping)

L7 ANSWER 27 OF 46 USPATFULL on STN
ACCESSION NUMBER: 2005:98935 USPATFULL
TITLE: Method
INVENTOR(S): Ronaghi, Mostafa, Palo Alto, CA, UNITED STATES
Ekstorm, Bjorn, Uppsala, SWEDEN
Pourmand, Nader, Palo Alto, CA, UNITED STATES

	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 2005084851	A1	20050421	
APPLICATION INFO.:	US 2003-363177	A1	20010910	(10)
	WO 2001-GB4042		20010910	

	NUMBER	DATE
PRIORITY INFORMATION:	GB 2003-22069	20000908

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: DORSEY & WHITNEY LLP, INTELLECTUAL PROPERTY DEPARTMENT, 250 PARK AVENUE, NEW YORK, NY, 10177, US
NUMBER OF CLAIMS: 15
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 19 Drawing Page(s)
LINE COUNT: 2257
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The method of the invention relates to a method of typing one or more nucleic acid molecules, said method comprising: simultaneously or sequentially performing two or more primer extension reactions, each primer binding at a different predetermined site in said nucleic acid molecule(s), and determining the pattern of nucleotide incorporation to obtain a test pattern for said nucleic acid molecule(s) which is optionally compared with one or more reference patterns to type the said nucleic acid molecule(s).

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
IT **404321-95-5**
(unclaimed nucleotide sequence; multiplex primer extension method of DNA fingerprinting for rapid identification)

L7 ANSWER 28 OF 46 USPATFULL on STN
ACCESSION NUMBER: 2005:68861 USPATFULL
TITLE: Method of stabilizing reagent for amplifying or detecting nucleic acid and storage method
INVENTOR(S): Sagawa, Hiroaki, Kusatsu-shi, JAPAN
Uemori, Takashi, Otsu-shi, JAPAN
Mukai, Hiroyuki, Moriyama-shi, JAPAN
Yamamoto, Junko, Moriyama-shi, JAPAN
Tomono, Jun, Kusatsu-shi, JAPAN
Kobayashi, Eiji, Otsu-shi, JAPAN
Enoki, Tatsuji, Otsu-shi, JAPAN
Asada, Kiyozo, Koka-gun, JAPAN
Kato, Ikunoshin, Koka-gun, JAPAN

	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 2005059000	A1	20050317	
APPLICATION INFO.:	US 2003-478633	A1	20031125	(10)

WO 2002-JP5832 20020612

	NUMBER	DATE
PRIORITY INFORMATION:	JP 2001-177737	20010612

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: BROWDY AND NEIMARK, P.L.L.C., 624 NINTH STREET, NW, SUITE 300, WASHINGTON, DC, 20001-5303
NUMBER OF CLAIMS: 11
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 7 Drawing Page(s)
LINE COUNT: 4503
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A method of stabilizing a reaction reagent for highly sensitively and specifically amplifying a target nucleic acid in a sample with the use of a chimeric oligonucleotide primer and a method of storing the same over a long time; and a method of highly sensitively detecting a pathogenic microorganism and a virus.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
IT [illegible]
(unclaimed nucleotide sequence; oligonucleotide probes and primers for detecting pathogenic microorganism)

L7 ANSWER 29 OF 46 USPATFULL on STN
ACCESSION NUMBER: 2005:68843 USPATFULL
TITLE: Modified small interfering RNA molecules and methods of use
INVENTOR(S): Han, Jang, Lafayette, CA, UNITED STATES
Seo, Mi-Young, Bucheon-si, KOREA, REPUBLIC OF
Houghton, Michael, Danville, CA, UNITED STATES
PATENT ASSIGNEE(S): Chiron Corporation (U.S. corporation)

	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 2005058982	A1	20050317	
APPLICATION INFO.:	US 2003-626879	A1	20030725	(10)

	NUMBER	DATE
PRIORITY INFORMATION:	US 2003-470230P	20030514 (60)
	US 2003-461838P	20030411 (60)
	US 2002-398605P	20020726 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: Chiron Corporation, Intellectual Property - R440, P.O. Box 8097, Emeryville, CA, 94662-8097
NUMBER OF CLAIMS: 66
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 24 Drawing Page(s)
LINE COUNT: 2189
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention provides double-stranded RNA molecules that mediate RNA interference in target cells, preferably hepatic cells. The invention also provides double-stranded RNA molecules that are modified to be resistant to nuclease degradation, which inactivates a virus, and more specifically, hepatitis C virus (HCV). The invention also provides a method of using these modified RNA molecules to inactivate virus in mammalian cells and a method of making modified small interfering RNAs

(siRNAs) using human Dicer.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
IT **654887-99-7**
(unclaimed sequence; small interfering RNAs with backbone or base modifications directed against hepatitis C virus and their use in treatment of infection)

L7 ANSWER 30 OF 46 USPATFULL on STN

ACCESSION NUMBER:	2004:247173 USPATFULL
TITLE:	Process for typing of HCV isolates
INVENTOR(S):	Maertens, Geert, Brugge, BELGIUM Stuyver, Lieven, Borsbeke, BELGIUM Rossau, Rudi, Ekeren, BELGIUM Van Heuverswyn, Hugo, Kalken, BELGIUM
PATENT ASSIGNEE(S):	INNOGENETICS, S.A., Ghent, BELGIUM (non-U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2004191768	A1	20040930
APPLICATION INFO.:	US 2004-822711	A1	20040413 (10)

RELATED APPLN. INFO.: Division of Ser. No. US 2001-899082, filed on 6 Jul 2001, PENDING Division of Ser. No. US 1999-378900, filed on 23 Aug 1999, GRANTED, Pat. No. US 6495670 Division of Ser. No. US 1998-44665, filed on 19 Mar 1998, GRANTED, Pat. No. US 6051696 Division of Ser. No. US 1994-256568, filed on 18 Jul 1994, GRANTED, Pat. No. US 5846704 A 371 of International Ser. No. WO 1993-EP3325, filed on 26 Nov 1993, UNKNOWN

	NUMBER	DATE
PRIORITY INFORMATION:	EP 1992-403222	19921127
	EP 1993-402129	19930831

DOCUMENT TYPE:	Utility
FILE SEGMENT:	APPLICATION
LEGAL REPRESENTATIVE:	NIXON & VANDERHYE, PC, 1100 N GLEBE ROAD, 8TH FLOOR, ARLINGTON, VA, 22201-4714
NUMBER OF CLAIMS:	23
EXEMPLARY CLAIM:	1
NUMBER OF DRAWINGS:	17 Drawing Page(s)
LINE COUNT:	4218

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The invention relates to a process for genotyping any HCV isolate present in a biological sample, previously identified as being HCV positive, and for classifying said isolate according to the percentage of homology with other HCV isolates, comprising the steps of:

contacting said sample in which the ribonucleotides or deoxyribonucleotides have been made accessible, if need be, under suitable denaturation, with at least one probe from about 10 to about 40 nucleotides, with said probe being liable to hybridize to a region being in the domain extending from nucleotide at position -291 to nucleotide at position -66 of the 5' untranslated region of one of the HCV isolates represented by their cDNA sequences, with said numbering of position beginning with the first ATG codon of the open reading frame encoding the HCV polyprotein, or with said probe being complementary to the above-defined probes,

detecting the complexes possibly formed between said probe and the nucleotide sequence of the HCV isolate to be identified.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
IT 157607-57-3
(PCR primer for amplification of 5'-untranslated region of hepatitis C virus RNA, typing of virus by hybridization in relation to)

L7 ANSWER 31 OF 46 USPATFULL on STN

ACCESSION NUMBER:	2004:239649 USPATFULL			
TITLE:	Method of detecting pathogenic microorganism			
INVENTOR(S):	Shimada, Masamitsu, Otsu-shi, JAPAN			
	Hino, Fumitsugu, Kusatsu-shi, JAPAN			
	Kato, Ikunoshin, Uji-shi, JAPAN			
	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 2004185455	A1	20040923	
APPLICATION INFO.:	US 2003-451882	A1	20030626	(10)
	WO 2001-JP11422		20011226	
	NUMBER		DATE	
PRIORITY INFORMATION:	JP 2000-396222		20001226	
	JP 2000-396321		20001226	
	JP 2001-199552		20010629	
	JP 2001-278920		20010913	
DOCUMENT TYPE:	Utility			
FILE SEGMENT:	APPLICATION			
LEGAL REPRESENTATIVE:	BROWDY AND NEIMARK, P.L.L.C., 624 NINTH STREET, NW, SUITE 300, WASHINGTON, DC, 20001-5303			
NUMBER OF CLAIMS:	77			
EXEMPLARY CLAIM:	1			
NUMBER OF DRAWINGS:	1 Drawing Page(s)			
LINE COUNT:	3180			

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Oligonucleotide probes and primers useful in detecting pathogenic microorganisms; a method of detecting a pathogenic microorganism by using the same; and kits for this method.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
IT 440077-63-4
(unclaimed nucleotide sequence; oligonucleotide probes and primers for detecting pathogenic microorganism)

L7 ANSWER 32 OF 46 USPATFULL on STN

ACCESSION NUMBER:	2004:178285 USPATFULL			
TITLE:	Method of detecting nucleotide polymorphism			
INVENTOR(S):	Sagawa, Hiroaki, Shiga, JAPAN			
	Kobayashi, Eiji, Shiga, JAPAN			
	Kato, Ikunoshin, Kyoto, JAPAN			
	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 2004137451	A1	20040715	
APPLICATION INFO.:	US 2003-468128	A1	20030815	(10)
	WO 2002-JP1222		20020214	
	NUMBER		DATE	

PRIORITY INFORMATION: JP 2001-39268 20010215
JP 2001-40721 20010216
JP 2001-101055 20010330
JP 2001-177381 20010612
JP 2001-290384 20010925
JP 2001-338440 20011102
JP 2001-368929 20011203
DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: BROWDY AND NEIMARK, P.L.L.C., 624 NINTH STREET, NW, SUITE 300, WASHINGTON, DC, 20001-5303
NUMBER OF CLAIMS: 39
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 8 Drawing Page(s)
LINE COUNT: 1770
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A Nucleotide useful for detecting a base substitution in a gene, a method for detecting a base substitution in a gene using said Nucleotide, and a kit for the same.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
IT **440077-63-4**
(unclaimed nucleotide sequence; oligonucleotide probes and primers for detecting pathogenic microorganism)

L7 ANSWER 33 OF 46 USPATFULL on STN
ACCESSION NUMBER: 2004:178258 USPATFULL
TITLE: Nucleic acids and methods for detecting viral infection, uncovering anti-viral drug candidates and determining drug resistance of viral isolates
INVENTOR(S): Tan, Yin Hwee, St Vancouver, CANADA
Lim, Siew Pheng, Singapore, SINGAPORE
Lim, Seng Gee, Singapore, SINGAPORE

	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 2004137424	A1	20040715	
APPLICATION INFO.:	US 2003-333449	A1	20030804	(10)
	WO 2001-IL669		20010720	

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: WILDMAN, HARROLD, ALLEN & DIXON, 225 WEST WACKER DRIVE, CHICAGO, IL, 60606
NUMBER OF CLAIMS: 43
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 6 Drawing Page(s)
LINE COUNT: 1533
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A nucleic acid construct is provided. The nucleic acid construct includes an expression cassette including: a first polynucleotide region including a 5' NCR sequence of an RNA virus and at least an N-terminal portion of a core sequence of the RNA virus; a second polynucleotide region including a 3' UTR sequence of the RNA virus and at least a C-terminal portion of a polymerase sequence of the virus; and a third polynucleotide region encoding a reporter molecule, the third polynucleotide region being flanked by the first and the second polynucleotide regions; and a promoter sequence being operatively linked to the expression cassette in a manner so as to enable a transcription of a minus strand RNA molecule from the expression cassette.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
IT 393599-90-1
(unclaimed nucleotide sequence; nucleic acid construct and methods for detecting RNA viral infection, screening for anti-viral drug and determining drug resistance of isolated virus)

L7 ANSWER 34 OF 46 USPATFULL on STN

ACCESSION NUMBER:	2004:151497 USPATFULL
TITLE:	Method of assay of target nucleic acid
INVENTOR(S):	Ishiguro, Takahiko, Kanagawa, JAPAN Saitoh, Juichi, Kanagawa, JAPAN Ishizuka, Tetsuya, Kanagawa, JAPAN
PATENT ASSIGNEE(S):	TOSOH CORPORATION (non-U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2004115718	A1	20040617
APPLICATION INFO.:	US 2003-687588	A1	20031020 (10)
RELATED APPLN. INFO.:	Continuation of Ser. No. US 1999-345761, filed on 1 Jul 1999, ABANDONED		

	NUMBER	DATE
PRIORITY INFORMATION:	JP 1998-186434	19980701

DOCUMENT TYPE:	Utility
FILE SEGMENT:	APPLICATION
LEGAL REPRESENTATIVE:	SUGHRUE MION, PLLC, 2100 PENNSYLVANIA AVENUE, N.W., SUITE 800, WASHINGTON, DC, 20037
NUMBER OF CLAIMS:	28
EXEMPLARY CLAIM:	1
NUMBER OF DRAWINGS:	10 Drawing Page(s)
LINE COUNT:	1889

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB A simple and accurate method for assay of a single-stranded RNA containing a specific nucleic acids sequence in a sample at almost constant temperature by using at least the following reagents (A) to (I), which comprises a step of adding the reagents (A) to (I) one by one (in any order), in combinations of at least two or all at once and

a step of measuring a fluorescent signal in the presence of the reagent (I) at least once after addition of at least the reagents (A) to (H);

(A) a first single-stranded oligonucleic acid complementary to a sequence neighboring the 5' end of the specific nucleic acids sequence in the single-stranded RNA,

(B) a second single-stranded oligo DNA complementary to a 3'-end sequence within the specific nucleic acids sequence,

(C) an RNA-dependent DNA polymerase,

(D) deoxyribonucleoside triphosphates,

(E) a third single-stranded oligo DNA having (1) a promoter sequence for a DNA-dependent RNA polymerase, (2) an enhancer sequence for the promoter and (3) a 5'-end sequence within the specific nucleic acids sequence, in this order from the 5' end,

(F) a DNA-dependent DNA polymerase,

(G) a DNA-dependent RNA polymerase,

(H) ribonucleoside triphosphates, and

(I) a fourth single-stranded oligo DNA complementary to the specific nucleic acids sequence which is labeled so that it gives off a measurable fluorescent signal on hybridization with a nucleic acid containing the specific nucleic acids sequence.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
IT **253656-91-6**
(unclaimed nucleotide sequence; isothermal amplification method for the detection of a specific RNA)

L7 ANSWER 35 OF 46 USPATFULL on STN
ACCESSION NUMBER: 2004:94696 USPATFULL
TITLE: Simultaneous detection of HBV, HCV, and HIV in plasma samples using a multiplex capture assay
INVENTOR(S): Ji, Jiuping, Rockville, MD, UNITED STATES
Manak, Mark, Laurel, MD, UNITED STATES
Gonzalez, Irene, Baltimore, MD, UNITED STATES

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2004072148	A1	20040415
APPLICATION INFO.:	US 2003-407897	A1	20030407 (10)

RELATED APPLN. INFO.: Continuation of Ser. No. US 130533, PENDING A 371 of International Ser. No. WO 2000-US31738, filed on 17 Nov 2000, PENDING

	NUMBER	DATE
PRIORITY INFORMATION:	US 1999-165916P	19991117 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: STERNE, KESSLER, GOLDSTEIN & FOX PLLC, 1100 NEW YORK AVENUE, N.W., WASHINGTON, DC, 20005
NUMBER OF CLAIMS: 46
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 3 Drawing Page(s)
LINE COUNT: 1646
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention is directed to a capture assay to simultaneously screen for HBV, HCV and HIV nucleic acids in samples such as plasma. The nucleic acids including both viral DNA and RNA are purified from the plasma samples in a single extraction procedure. In one embodiment, a mixture of degenerate biotin-labelled PCR primers specific for the HBV, HCV, HIV-1 type M and HIV-1 type O are used to amplify any of these viruses which may be present in plasma. Amplified products are captured by hybridization to immobilized capture sequence, and thereafter detected. An internal control vector containing a synthetic fragment flanked by sequences corresponding to the HBV primers was designed to monitor sample recovery during extraction, amplification and detection. All major subtypes of HBV, HCV and HIV including HIV-1 type O have been confirmed and detected by the assay.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
IT **157607-57-3**
(unclaimed sequence; simultaneous detection of HBV, HCV and HIV in plasma samples using a multiplex capture assay by PCR and RT-PCR)

L7 ANSWER 36 OF 46 USPATFULL on STN
ACCESSION NUMBER: 2004:57377 USPATFULL
TITLE: Method of detectingnucleic acid relating to disease
INVENTOR(S): Hashimoto, Koji, Kanagawa, JAPAN
Hashimoto, Michie, Tokyo, JAPAN
Mishiro, Shunji, Tokyo, JAPAN
Oota, Yasuhiko, Tokyo, JAPAN

	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 2004043379	A1	20040304	
APPLICATION INFO.:	US 2003-70415	A1	20030129	(10)
	WO 2002-JP2030		20020305	

	NUMBER	DATE
PRIORITY INFORMATION:	JP 2001-90053	20010327
	JP 2001-284112	20010918

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C., 1940 DUKE STREET, ALEXANDRIA, VA, 22314
NUMBER OF CLAIMS: 33
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 1 Drawing Page(s)
LINE COUNT: 3026
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention provides methods for obtaining information regarding nucleic acid from an individual and nucleic acid associated with a disease of the individual, in particular when the disease is associated with a pathogenic microorganism present within the individual. The present invention also provide probe-immobilized substrates, such as probe-immobilized chips, for use in the methods. In particular, the present invention provides methods and probe-immobilized substrates for obtaining information regarding responsiveness to a treatment for a disease of an individual.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
IT 465577-45-1
(nucleic acid sequence; probes and SNP in human protein MxA and mannose binding lectin gene for diagnosis of hepatitis C)

L7 ANSWER 37 OF 46 USPATFULL on STN
ACCESSION NUMBER: 2003:51096 USPATFULL
TITLE: Process for typing HCV isolates
INVENTOR(S): Maertens, Geert, Brugge, BELGIUM
Stuyver, Lieven, Borsbeke, BELGIUM
Rossau, Rudi, Ekeren, BELGIUM
Van Heuverswyn, Hugo, Kalken, BELGIUM
PATENT ASSIGNEE(S): Innogenetics N.V. (non-U.S. corporation)

	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 2003036053	A1	20030220	
	US 6548244	B2	20030415	
APPLICATION INFO.:	US 2001-899044	A1	20010706	(9)

RELATED APPLN. INFO.: Division of Ser. No. US 1999-378900, filed on 23 Aug 1999, PENDING Division of Ser. No. US 1998-44665, filed on 19 Mar 1998, PATENTED

	NUMBER	DATE
PRIORITY INFORMATION:	EP 1992-403222	19921127
	EP 1993-402129	19930831
	WO 1993-EP3325	19931126

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: NIXON & VANDERHYE P.C., 8th Floor, 1100 North Glebe Rd., Arlington, VA, 22201-4714
NUMBER OF CLAIMS: 23
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 14 Drawing Page(s)
LINE COUNT: 4191
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The invention relates to a process for genotyping any HCV isolate present in a biological sample, previously identified as being HCV positive, and for classifying said isolate according to the percentage of homology with other HCV isolates, comprising the steps of:

contacting said sample in which the ribonucleotides or deoxyribonucleotides have been made accessible, if need be, under suitable denaturation, with at least one probe from about 10 to about 40 nucleotides, with said probe being liable to hybridize to a region being in the domain extending from nucleotide at position -291 to nucleotide at position -66 of the 5' untranslated region of one of the HCV isolates represented by their cDNA sequences, with said numbering of position beginning with the first ATG codon of the open reading frame encoding the HCV polyprotein, or with said probe being complementary to the above-defined probes,

detecting the complexes possibly formed between said probe and the nucleotide sequence of the HCV isolate to be identified.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
IT **157607-57-3**
(PCR primer for amplification of 5'-untranslated region of hepatitis C virus RNA, typing of virus by hybridization in relation to)

L7 ANSWER 38 OF 46 USPATFULL on STN
ACCESSION NUMBER: 2002:301083 USPATFULL
TITLE: Process for typing of HCV isolates
INVENTOR(S): Maertens, Geert, Brugge, BELGIUM
Stuyver, Lieven, Borsbeke, BELGIUM
Rossau, Rudi, Ekeren, BELGIUM
Van Heuverswyn, Hugo, Kalken, BELGIUM
PATENT ASSIGNEE(S): Innogenetics N.V. (non-U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2002168626	A1	20021114
	US 6887985	B2	20050503
APPLICATION INFO.:	US 2001-899302	A1	20010706 (9)

RELATED APPLN. INFO.: Division of Ser. No. US 1999-378900, filed on 23 Aug 1999, PENDING Division of Ser. No. US 1998-44665, filed on 19 Mar 1998, GRANTED, Pat. No. US 6051696

	NUMBER	DATE
PRIORITY INFORMATION:	EP 1992-403222	19921127

EP 1993-402129 19930831
WO 1993-EP3325 19931126
DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: NIXON & VANDERHYE P.C., 8th Floor, 1100 North Glebe Rd., Arlington, VA, 22201-4714
NUMBER OF CLAIMS: 23
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 14 Drawing Page(s)
LINE COUNT: 4138
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention relates to a process for genotyping any HCV isolate present in a biological sample, previously identified as being HCV positive, and for classifying said isolate according to the percentage of homology with other HCV isolates, comprising the steps of:

contacting said sample in which the ribonucleotides or deoxyribonucleotides have been made accessible, if need be, under suitable denaturation, with at least one probe from about 10 to about 40 nucleotides, with said probe being liable to hybridize to a region being in the domain extending from nucleotide at position -291 to nucleotide at position -66 of the 5' untranslated region of one of the HCV isolates represented by their cDNA sequences, with said numbering of position beginning with the first ATG codon of the open reading frame encoding the HCV polyprotein, or with said probe being complementary to the above-defined probes,

detecting the complexes possibly formed between said probe and the nucleotide sequence of the HCV isolate to be identified.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
IT 157607-57-3
(PCR primer for amplification of 5'-untranslated region of hepatitis C virus RNA, typing of virus by hybridization in relation to)

L7 ANSWER 39 OF 46 USPATFULL on STN
ACCESSION NUMBER: 2002:251096 USPATFULL
TITLE: 5' Nuclease nucleic acid amplification assay having an improved internal control
INVENTOR(S): Gessner, Matthias, Gross Enzersdorf, AUSTRIA
PATENT ASSIGNEE(S): Baxter Aktiengesellschaft (non-U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2002137039	A1	20020926
APPLICATION INFO.:	US 2000-746874	A1	20001222 (9)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: John P. Isacson, HELLER, EHRMAN, WHITE & McAULIFFE LLP, 1666 K Street NW, Suite 300, Washington,, DC, 20006-1228
NUMBER OF CLAIMS: 20
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 1 Drawing Page(s)
LINE COUNT: 1096
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Nucleic acid amplification assays using a 5' nuclease and having internal amplification controls are provided. Related methods for preparing the internal controls are also provided. Moreover, methods for rapidly and accurately determining optimum nucleic acid sequences for

the internal amplification controls the 5' nuclease assays are provided.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
IT **439889-66-4**
(unclaimed nucleotide sequence; method of generating an improved internal control for diagnosis of viral infections using a 5' nuclease PCR assay)

L7 ANSWER 40 OF 46 USPATFULL on STN

ACCESSION NUMBER:	2002:198538 USPATFULL		
TITLE:	Process for typing of HCV isolates		
INVENTOR(S):	Maertens, Geert, Brugge, BELGIUM Stuyver, Lieven, Borsbeke, BELGIUM Rossau, Rudi, Ekeren, BELGIUM Van Heuverswyn, Hugo, Kalken, BELGIUM		
PATENT ASSIGNEE(S):	Innogenetics N.V. (non-U.S. corporation)		
	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2002106638	A1	20020808
	US 6891026	B2	20050510
APPLICATION INFO.:	US 2001-899082	A1	20010706 (9)
RELATED APPLN. INFO.:	Division of Ser. No. US 1999-378900, filed on 23 Aug 1999, PENDING Division of Ser. No. US 1998-44665, filed on 19 Mar 1998, PATENTED		
	NUMBER		DATE
PRIORITY INFORMATION:	EP 1992-403222		19921127
	EP 1993-402129		19930831
DOCUMENT TYPE:	Utility		
FILE SEGMENT:	APPLICATION		
LEGAL REPRESENTATIVE:	NIXON & VANDERHYE P.C., 8th Floor, 1100 North Glebe Rd., Arlington, VA, 22201-4714		
NUMBER OF CLAIMS:	23		
EXEMPLARY CLAIM:	1		
NUMBER OF DRAWINGS:	14 Drawing Page(s)		
LINE COUNT:	4235		

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention relates to a process for genotyping any HCV isolate present in a biological sample, previously identified as being HCV positive, and for classifying said isolate according to the percentage of homology with other HCV isolates, comprising the steps of:

contacting said sample in which the ribonucleotides or deoxyribonucleotides have been made accessible, if need be, under suitable denaturation, with at least one probe from about 10 to about 40 nucleotides, with said probe being liable to hybridize to a region being in the domain extending from nucleotide at position -291 to nucleotide at position -66 of the 5' untranslated region of one of the HCV isolates represented by their cDNA sequences, with said numbering of position beginning with the first ATG codon of the open reading frame encoding the HCV polyprotein, or with said probe being complementary to the above-defined probes,

detecting the complexes possibly formed between said probe and the nucleotide sequence of the HCV isolate to be identified.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
IT **157607-57-3**

(PCR primer for amplification of 5'-untranslated region of hepatitis C virus RNA, typing of virus by hybridization in relation to)

L7 ANSWER 41 OF 46 USPATFULL on STN
ACCESSION NUMBER: 2002:126266 USPATFULL
TITLE: Primer-specific and mispair extension assay for identifying gene variation
INVENTOR(S): Hu, Yu-Wen, Gloucester, CANADA

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2002064778	A1	20020530
	US 6811974	B2	20041102
APPLICATION INFO.:	US 2001-782361	A1	20010213 (9)

RELATED APPLN. INFO.: Continuation of Ser. No. WO 1999-CA733, filed on 9 Aug 1999, UNKNOWN

	NUMBER	DATE
PRIORITY INFORMATION:	CA 1998-2245039	19980813

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: TRASK BRITT, P.O. BOX 2550, SALT LAKE CITY, UT, 84110
NUMBER OF CLAIMS: 12
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 10 Drawing Page(s)
LINE COUNT: 1417
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention relates to primer-specific and mispair extension assays for identifying gene variations, such as in different genotypes or subtypes of a given genotype. The assay includes extending a nucleic acid sequence from a patient sample with extension products of the primer, characterizing the extension products, and comparing the extension products with known nucleic acid sequences of various genotypes for determining the genotype of the nucleic acid sequence extended. In the assay, at least one primer or the dNTPs is labeled.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
IT 259204-93-8,
(sense universal PCR primer (first round); primer-specific and mispair extension assay (PSMEA) used for genotyping hepatitis C virus)

L7 ANSWER 42 OF 46 USPATFULL on STN
ACCESSION NUMBER: 2002:332818 USPATFULL
TITLE: Process for typing of HCV isolates
INVENTOR(S): Maertens, Geert, Brugge, BELGIUM
Stuyver, Lieven, Borsbeke, BELGIUM
Rossau, Rudi, Ekeren, BELGIUM
Van Heuverswyn, Hugo, Kalken, BELGIUM
PATENT ASSIGNEE(S): Innogenetics, N.V., Ghent, BELGIUM (non-U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 6495670	B1	20021217
APPLICATION INFO.:	US 1999-378900		19990823 (9)

RELATED APPLN. INFO.: Division of Ser. No. US 1998-44665, filed on 19 Mar 1998, now patented, Pat. No. US 6051696 Division of Ser. No. US 256568, now patented, Pat. No. US 5846704

	NUMBER	DATE
PRIORITY INFORMATION:	EP 1992-403222	19921127
	EP 1993-402129	19930831

DOCUMENT TYPE: Utility
FILE SEGMENT: GRANTED
PRIMARY EXAMINER: Whisenant, Ethan C.
LEGAL REPRESENTATIVE: Nixon & Vanderhye, P.C.
NUMBER OF CLAIMS: 7
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 16 Drawing Figure(s); 14 Drawing Page(s)
LINE COUNT: 3572
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The invention relates to a process for genotyping any HCV isolate present in a biological sample, previously identified as being HCV positive, and for classifying said isolate according to the percentage of homology with other HCV isolates, comprising the steps of:

contacting said sample in which the ribonucleotides or deoxyribonucleotides have been made accessible, if need be, under suitable denaturation, with at least one probe from about 10 to about 40 nucleotides, with said probe being liable to hybridize to a region being in the domain extending from nucleotide at position -291 to nucleotide at position -66 of the 5' untranslated region of one of the HCV isolates represented by their cDNA sequences, with said numbering of position beginning with the first ATG codon of the open reading frame encoding the HCV polyprotein, or with said probe being complementary to the above-defined probes,

detecting the complexes possibly formed between said probe and the nucleotide sequence of the HCV isolate to be identified.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
IT **157607-57-3**
(PCR primer for amplification of 5'-untranslated region of hepatitis C virus RNA, typing of virus by hybridization in relation to)

L7 ANSWER 43 OF 46 USPATFULL on STN
ACCESSION NUMBER: 2001:233290 USPATFULL
TITLE: METHOD OF ASSAY OF TARGET NUCLEIC ACID
INVENTOR(S): ISHIGURO, TAKAHIKO, KANAGAWA, Japan
SAITOH, JUICHI, KANAGAWA, Japan
ISHIZUKA, TETSUYA, KANAGAWA, Japan

	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 2001053518	A1	20011220	
APPLICATION INFO.:	US 1999-345761	A1	19990701	(9)

	NUMBER	DATE
PRIORITY INFORMATION:	JP 1998-186434	19980701

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: SUGHRUE MION ZINN, MACPEAK & SEAS PLLC, 2100 PENNSYLVANIA AVENUE NW, WASHINGTON, DC, 200373202
NUMBER OF CLAIMS: 28
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 16 Drawing Page(s)
LINE COUNT: 1848

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB A simple and accurate method for assay of a single-stranded RNA containing a specific nucleic acids sequence in a sample at almost constant temperature by using at least the following reagents (A) to (I), which comprises a step of adding the reagents (A) to (I) one by one (in any order), in combinations of at least two or all at once and

a step of measuring a fluorescent signal in the presence of the reagent (I) at least once after addition of at least the reagents (A) to (H);

(A) a first single-stranded oligonucleic acid complementary to a sequence neighboring the 5' end of the specific nucleic acids sequence in the single-stranded RNA,

(B) a second single-stranded oligo DNA complementary to a 3'-end sequence within the specific nucleic acids sequence,

(C) an RNA-dependent DNA polymerase,

(D) deoxyribonucleoside triphosphates,

(E) a third single-stranded oligo DNA having (1) a promoter sequence for a DNA-dependent RNA polymerase, (2) an enhancer sequence for the promoter and (3) a 5'-end sequence within the specific nucleic acids sequence, in this order from the 5' end,

(F) a DNA-dependent DNA polymerase,

(G) a DNA-dependent RNA polymerase,

(H) ribonucleoside triphosphates, and

(I) a fourth single-stranded oligo DNA complementary to the specific nucleic acids sequence which is labeled so that it gives off a measurable fluorescent signal on hybridization with a nucleic acid containing the specific nucleic acids sequence.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

IT 253656-91-6
(unclaimed nucleotide sequence; isothermal amplification method for the detection of a specific RNA)

L7 ANSWER 44 OF 46 USPATFULL on STN

ACCESSION NUMBER:	2001:4458 USPATFULL
TITLE:	Process for typing of HCV isolates
INVENTOR(S):	Maertens, Geert, Brugge, Belgium Stuyver, Lieven, Borsbeke, Belgium Rossau, Rudi, Ekeren, Belgium Van Heuverswyn, Hugo, Kalken, Belgium
PATENT ASSIGNEE(S):	N.V. Innogenetics S.A., Belgium (non-U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 6171784	B1	20010109
APPLICATION INFO.:	US 1998-38369		19980310 (9)
RELATED APPLN. INFO.:	Continuation of Ser. No. US 258568, now patented, Pat. No. US 5846704		

	NUMBER	DATE

PRIORITY INFORMATION: EP 1992-403222 19921127
EP 1993-402129 19930831
DOCUMENT TYPE: Patent
FILE SEGMENT: Granted
PRIMARY EXAMINER: Fredman, Jeffrey
ASSISTANT EXAMINER: Einsmann, Juliet C.
LEGAL REPRESENTATIVE: Bierman, Muserlian & Lucas
NUMBER OF CLAIMS: 2
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 17 Drawing Figure(s); 17 Drawing Page(s)
LINE COUNT: 2518
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention relates to a process for genotyping any HCV isolate present in a biological sample, previously identified as being HCV positive, and for classifying said isolate according to the percentage of homology with other HCV isolates, comprising the steps of:

contacting said sample in which the ribonucleotides or deoxyribonucleotides have been made accessible, if need be, under suitable denaturation, with at least one probe from about 10 to about 40 nucleotides, with said probe being liable to hybridize to a region being in the domain extending from nucleotide at position -291 to nucleotide at position -66 of the 5' untranslated region of one of the HCV isolates represented by their cDNA sequences, with said numbering of position beginning with the first ATG codon of the open reading frame encoding the HCV polyprotein, or with said probe being complementary to the above-defined probes,

detecting the complexes possibly formed between said probe and the nucleotide sequence of the HCV isolate to be identified.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
IT **157607-57-3**
(PCR primer for amplification of 5'-untranslated region of hepatitis C virus RNA, typing of virus by hybridization in relation to)

L7 ANSWER 45 OF 46 USPATFULL on STN
ACCESSION NUMBER: 2000:47353 USPATFULL
TITLE: Process for typing of HCV isolates
INVENTOR(S): Maertens, Geert, Bruges, Belgium
Stuyver, Lieven, Borsbeke, Belgium
Rossau, Rudi, Ekeren, Belgium
Van Heuverswyn, Hugo, Kalken, Belgium
PATENT ASSIGNEE(S): N.V. Innogenetics S.A., Belgium (non-U.S. corporation)

	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 6051696		20000418	
APPLICATION INFO.:	US 1998-44665		19980319	(9)
RELATED APPLN. INFO.:	Division of Ser. No. US 256568			

	NUMBER	DATE
PRIORITY INFORMATION:	EP 1992-403222	19921127
	EP 1993-402129	19930831

DOCUMENT TYPE: Utility
FILE SEGMENT: Granted
PRIMARY EXAMINER: Jones, W. Gary
ASSISTANT EXAMINER: Whisenant, Ethan
LEGAL REPRESENTATIVE: Bierman, Muserlian and Lucas

NUMBER OF CLAIMS: 2
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 16 Drawing Figure(s); 14 Drawing Page(s)
LINE COUNT: 3944
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention relates to a process for genotyping any HCV isolate present in a biological sample, previously identified as being HCV positive, and for classifying said isolate according to the percentage of homology with other HCV isolates, comprising the steps of:

contacting said sample in which the ribonucleotides or deoxyribonucleotides have been made accessible, if need be, under suitable denaturation, with at least one probe from about 10 to about 40 nucleotides, with said probe being liable to hybridize to a region being in the domain extending from nucleotide at position -291 to nucleotide at position -66 of the 5' untranslated region of one of the HCV isolates represented by their cDNA sequences, with said numbering of position beginning with the first ATG codon of the open reading frame encoding the HCV polyprotein, br with said probe being complementary to the above-defined probes,

detecting the complexes possibly formed between said probe and the nucleotide sequence of the HCV isolate to be identified.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
IT 157607-57-3
(PCR primer for amplification of 5'-untranslated region of hepatitis C virus RNA, typing of virus by hybridization in relation to)

L7 ANSWER 46 OF 46 USPATFULL on STN
ACCESSION NUMBER: 1998:154022 USPATFULL
TITLE: Process for typing of HCV isolates
INVENTOR(S): Maertens, Geert, Brugge, Belgium
Stuyver, Lieven, Borsbeke, Belgium
Rossau, Rudi, Ekeren, Belgium
Van Heuverswyn, Hugo, Kalken, Belgium
PATENT ASSIGNEE(S): N.V. Innogenetics S.A., Belgium (non-U.S. corporation)

	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 5846704		19981208	
	WO 9412670		19940609	
APPLICATION INFO.:	US 1994-256568		19940718	(8)
	WO 1993-EP3325		19931126	
			19940718	PCT 371 date
			19940718	PCT 102(e) date

	NUMBER	DATE
PRIORITY INFORMATION:	EP 1992-403222	19921127
	EP 1993-402129	19930831

DOCUMENT TYPE: Utility
FILE SEGMENT: Granted
PRIMARY EXAMINER: Jones, W. Gary
ASSISTANT EXAMINER: Atzel, Amy
LEGAL REPRESENTATIVE: Bierman, Muserlian and Lucas
NUMBER OF CLAIMS: 13
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 16 Drawing Figure(s); 14 Drawing Page(s)
LINE COUNT: 3381

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A method of genotyping of HCV isolates using probes targeting sequences from the 5- untranslated region of HCV.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
IT **157607-57-3**
(PCR primer for amplification of 5'-untranslated region of hepatitis C virus RNA, typing of virus by hybridization in relation to)

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